Package ‘CoreGx’

May 7, 2024

Type Package

Title Classes and Functions to Serve as the Basis for Other ‘Gx’ Packages

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Description A collection of functions and classes which serve as the foundation for our lab's suite of R packages, such as 'PharmacoGx' and 'RadioGx'. This package was created to abstract shared functionality from other lab package releases to increase ease of maintainability and reduce code repetition in current and future 'Gx' suite programs. Major features include a 'CoreSet' class, from which 'RadioSet' and 'PharmacoSet' are derived, along with get and set methods for each respective slot. Additional functions related to fitting and plotting dose response curves, quantifying statistical correlation and calculating area under the curve (AUC) or survival fraction (SF) are included. For more details please see the included documentation, as well as:


VignetteBuilder knitr

VignetteEngine knitr::rmarkdown

biocViews Software, Pharmacogenomics, Classification, Survival

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    'CoreSet-class.R' 'CoreSet-accessors.R' 'CoreSet-utils.R'
    'DataMapper-class.R' 'LongTable-accessors.R'
    'LongTable-utils.R' 'LongTableDataMapper-class.R'
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    'TreatmentResponseExperiment-class.R' 'TREDataMapper-class.R'
    'adaptiveMatthewCor.R' 'aggregate-methods.R'
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    'datasets.R' 'deprecated.R' 'endoaggregate-methods.R'
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    'methods-coerce.R' 'methods-dim.R' 'methods-dimnames.R'
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Convenience function for converting R code to a call

Description

This is used to pass through unevaluated R expressions into subset and [], where they will be evaluated in the correct context.

Usage

.(. . .)
Arguments

... pairlist One or more R expressions to convert to calls.

Value

call An R call object containing the quoted expression.

Examples

.(sample_line1 == 'A2058')

assayToBumpyMatrix

Convert a LongTable assay into a BumpyMatrix object

Description

Convert a LongTable assay into a BumpyMatrix object

Usage

.assayToBumpyMatrix(LT, assay, rows, cols, sparse = TRUE)

Arguments

LT LongTable with assay to convert into BumpyMatrix
assay character(1) A valid assay name in LT, as returned by assayNames(LT).
rows character() The rownames associated with the assay rowKey
cols character() The names associated with the assay colKey
sparse logical(1) Should the BumpyMatrix be sparse (i.e., is the assay sparse).

Value

BumpyMatrix containing the data from assay.
.convertCSetMolecularProfilesToSE

CSet molecularProfiles from ESets to SEs

Description
Converts all ExpressionSet objects within the molecularProfiles slot of a CoreSet to SummarizedExperiments.

Usage
.convertCSetMolecularProfilesToSE(cSet)

Arguments
cSet S4 A CoreSet containing molecular data in ExpressionSets

Value
S4 A CoreSet containing molecular data in a SummarizedExperiments

.distancePointLine Calculate shortest distance between point and line

Description
This function calculates the shortest distance between a point and a line in 2D space.

Usage
.distancePointLine(x, y, a = 1, b = 1, c = 0)

Arguments
x x-coordinate of point
y y-coordinate of point
a numeric(1) The coefficient in line equation a * x + b * y + c = 0. Defaults to 1.
b numeric(1) The coefficient in line equation a * x + b * y + c = 0. Defaults to 1.
c numeric(1) The intercept in line equation a * x + b * y + c = 0. Defaults to 0.

Value
numeric The shortest distance between a point and a line.

Examples
.distancePointLine(0, 0, 1, -1, 1)
.distancePointSegment  
*Calculate shortest distance between point and line segment*

**Description**

This function calculates the shortest distance between a point and a line segment in 2D space.

**Usage**

```
.distancePointSegment(x, y, x1, y1, x2, y2)
```

**Arguments**

- `x`  
x-coordinate of point
- `y`  
y-coordinate of point
- `x1`  
x-coordinate of one endpoint of the line segment
- `y1`  
y-coordinate of line segment endpoint with x-coordinate `x1`
- `x2`  
x-coordinate of other endpoint of line segment
- `y2`  
y-coordinate of line segment endpoint with x-coordinate `x2`

**Value**

`numeric` The shortest distance between a point and a line segment

**Examples**

```
.distancePointSegment(0, 0, -1, 1, 1, -1)
```

---

.fitCurve2  
*Curve fitting via stats::optim L-BFGS-B with fall-back grid/pattern search if convergence is not achieved.*

**Description**

Function to fit curve via stats::optim
Usage

.fitCurve2(
  par,
  x,
  y,
  fn,
  loss,
  lower = -Inf,
  upper = Inf,
  precision = 1e-04,
  density = c(2, 10, 5),
  step = 0.5/density,
  ...
  loss_args = list(),
  span = 1,
  optim_only = FALSE,
  control = list(factr = 1e-08, ndeps = rep(1e-04, times = length(par)), trace = 0)
)

Arguments

par  numeric Vector of initial guesses for the parameters. For each index i of par, par[i] must be within the range (lower[i], upper[i]). If only a single upper or lower value is present, that range is used for all parameters in par.
x  numeric Values to evaluate fn for.
y  numeric Target output values to optimize fn against.
fn  function A function to optimize. Any fn arguments passed via ... will be treated as constant and removed from the optimization. It is assumed that the first argument is the x value to optimize over and any subsequent arguments are free parameters to be optimized. Transformed to be optim compatible via make_optim_function is the first argument isn't already par.
loss character(1) or function Either the name of one of the bundled loss functions (see details) or a custom loss function to compute for the output of fn over x.
lower numeric(1) Lower bound for parameters. Parallel to par.
upper numeric(1) Upper bound for parameters. Parallel to par.
precision numeric Smallest step size used in pattern search, once step size drops below this value, the search terminates.
density numeric How many points in the dimension of each parameter should be evaluated (density of the grid)
step numeric Initial step size for pattern search.
... pairlist Fall through arguments to fn.
loss_args list Additional argument to the loss function. These get passed to losses via do.call analogously to using ....
span numeric Can be safely kept at 1, multiplicative ratio for initial step size in pattern search. Must be larger than precision.
optim_only logical(1) Should the fall back methods when optim fails be skipped? Default is FALSE.

control list List of control parameters to pass to optim. See ?optim for details.

Details

TODO

Value

numeric Vector of optimal parameters for fn fit against y on the values of x.

Examples

```r
## Not run:
# Four parameter hill curve equation
hillEqn <- function(x, Emin, Emax, EC50, lambda) {
  (Emin + Emax * (x / EC50)^lambda) / (1 + (x / EC50)^lambda)
}
# Make some dummy data
doses <- rev(1000 / (2^(1:20)))
lambda <- 1
Emin <- 1
Emax <- 0.1
EC50 <- median(doses)
response <- hillEqn(doses, Emin=Emin, lambda=lambda, Emax=Emax, EC50=EC50)
response <- response + rnorm(length(response), sd=sd(response)*0.1) # add noise
# 3-parameter optimization
3par <- .fitCurve2(
  par=c(Emax, EC50, lambda),
  x=doses,
  y=nresponse,
  fn=hillEqn,
  Emin=Emin, # set this as constant in the function being optimized (via ...)
  loss=.normal_loss,
  loss_args=list(trunc=FALSE, n=1, scale=0.07),
  upper=c(1, max(doses), 6),
  lower=c(0, min(doses), 0)
)
# 2-parameter optimization
2par <- .fitCurve2(
  par=c(Emax, EC50),
  x=doses,
  y=nresponse,
  fn=hillEqn,
  Emin=Emin, # set this as constant in the function being optimized (via ...)
  lambda=1,
  loss=.normal_loss,
  loss_args=list(trunc=FALSE, n=1, scale=0.07),
  upper=c(1, max(doses)),
  lower=c(0, min(doses))
)
```
### .intersectList

#### Intersect A List of More Than Two Vectors

**Description**

Utility to find the intersection between a list of more than two vectors or lists. This function extends the native intersect function to work on two or more arguments.

**Usage**

`.intersectList(...)`

**Arguments**

`...`  
A list of or any number of vector-like objects of the same mode, which could also be operated on by the native R set operations

**Value**

A vector-like object of the same mode as the first argument, containing only the intersection common to all arguments to the function

**Examples**

```r
list1 <- list('a', 'b', 'c')
list2 <- list('a', 'c')
list3 <- list('a', 'c', 'd')
listAll <- .intersectList(list1, list2, list3)
listAll
```

---

### .longTableToSummarizedExperiment

#### Convert LongTable to gDR Style SummarizedExperiment

**Description**

Convert LongTable to gDR Style SummarizedExperiment

**Usage**

`.longTableToSummarizedExperiment(LT, assay_names)`
.symSetDiffList

Arguments

LT LongTable to convert to gDR SummarizedExperiment format.

assay_names character() Names to rename the assays to. These are assumed to be in the same order as assayNames(LT).

Value

SummarizedExperiment object with all assay from LT as BumpyMatrixes.

Description

The function finds the symmetric set differences between all the arguments, defined as Union(args) - Intersection(args)

Usage

.symSetDiffList(...)

Arguments

... A list of or any number of vector like objects of the same mode, which could also be operated on by the native R set operations

Value

A vector like object of the same mode as the first argument, containing only the symmetric set difference

Examples

list1 <- list('a', 'b', 'c')
list2 <- list('a', 'c')
list3 <- list('a', 'c', 'd')
listAll <- .symSetDiffList(list1, list2, list3)
listAll
**.unionList**  
*Utility to find the union between a list of more than two vectors or lists*

**Description**
This function extends the native union function to work on two or more arguments.

**Usage**
```r
.unionList(...)```

**Arguments**
```r
...
```
A list of or any number of vector like objects of the same mode, which could also be operated on by the native R set operations

**Value**
A vector like object of the same mode as the first argument, containing all the elements of all arguments passed to the function

**Examples**
```r
list1 <- list('a', 'b')
list2 <- list('a', 'c')
list3 <- list('c', 'd')
listAll <- .unionList(list1, list2, list3)
listAll```

---

**aggregate, data.table-method**  
*Functional S4 API for aggregation over a data.table object.*

**Description**
Compute a group-by operation over a data.table in a functional, pipe compatible format.

**Usage**
```r
## S4 method for signature 'data.table'
aggregate(
  x,
  by,
  ...,  
  subset = TRUE,
)```
nthread = 1,
progress = TRUE,
BPPARAM = NULL,
enlist = TRUE,
moreArgs = list()
)

Arguments

x data.table to compute aggregation over.
by character One or more valid column names in x to compute groups using.
... call One or more aggregations to compute for each group by in x. If you name
group calls, that will be the column name of the value in the resulting
data.table otherwise a default name will be parsed from the function name
and its first argument, which is assumed to be the name of the column being
aggregated over.
subset call An R call to evaluate before perfoming an aggregate. This allows you to
aggregate over a subset of columns in an assay but have it be assigned to the
parent object. Default is TRUE, which includes all rows. Passed through as the
i argument in [.data.table.
nthread numeric(1) Number of threads to use for split-apply-combine parallelization.
Uses BiocParallel::bplapply if nthread > 1 or you pass in BPPARAM. Does not
modify data.table threads, so be sure to use setDTthreads for reasonable nested
parallelism. See details for performance considerations.
progress logical(1) Display a progress bar for parallelized computations? Only works
if bpprogressbar<- is defined for the current BioCParallel back-end.
BPPARAM BiocParallelParam object. Use to customized the the parallization back-end
of bplapply. Note, nthread over-rides any settings from BPPARAM as long as
bpworkers<- is defined for that class.
enlist logical(1) Default is TRUE. Set to FALSE to evaluate the first call in ... within
data.table groups. See details for more information.
moreArgs list() A named list where each item is an argument one of the calls in ...
which is not a column in the table being aggregated. Use to further parameterize
you calls. Please note that these are not added to your aggregate calls unless you
specify the names in the call.

Details

This S4 method override the default aggregate method for a data.frame and as such you need to
call aggregate.data.frame directly to get the original S3 method for a data.table.

Use of Non-Standard Evaluation:
Arguments in ... are substituted and wrapped in a list, which is passed through to the j argument
of [.data.table internally. The function currently tries to build informative column names for
unnamed arguments in ... by appending the name of each function call with the name of its first
argument, which is assumed to be the column name being aggregated over. If an argument to ... is
named, that will be the column name of its value in the resulting data.table.
Enlisting:
The primary use case for enlist=FALSE is to allow computation of dependent aggregations, where the output from a previous aggregation is required in a subsequent one. For this case, wrap your call in \{ and assign intermediate results to variables, returning the final results as a list where each list item will become a column in the final table with the corresponding name. Name inference is disabled for this case, since it is assumed you will name the returned list items appropriately. A major advantage over multiple calls to aggregate is that the overhead of parallelization is paid only once even for complex multi-step computations like fitting a model, capturing its parameters, and making predictions using it. It also allows capturing arbitrarily complex calls which can be recomputed later using the \update, \TreatmentResponseExperiment-method. A potential disadvantage is increased RAM usage per thread due to storing intermediate values in variables, as well as any memory allocation overhead associate therewith.

Value
data.table of aggregated results with an aggregations attribute capturing metadata about the last aggregation performed on the table.
... call One or more aggregations to compute for each group by in x. If you name aggregation calls, that will be the column name of the value in the resulting data.table otherwise a default name will be parsed from the function name and its first argument, which is assumed to be the name of the column being aggregated over.

subset call An R call to evaluate before performing an aggregate. This allows you to aggregate over a subset of columns in an assay but have it be assigned to the parent object. Default is TRUE, which includes all rows. Passed through as the i argument in [.data.table.

nthread numeric(1) Number of threads to use for split-apply-combine parallelization. Uses BiocParallel::bplapply if nthread > 1 or you pass in BPPARAM. Does not modify data.table threads, so be sure to use setDTthreads for reasonable nested parallelism. See details for performance considerations.

progress logical(1) Display a progress bar for parallelized computations? Only works if bpprogressbar<- is defined for the current BiocParallel back-end.

BPPARAM BiocParallelParam object. Use to customize the the parallelization back-end of bplapply. Note, nthread over-rides any settings from BPPARAM as long as bpworkers<- is defined for that class.

tenlist logical(1) Default is TRUE. Set to FALSE to evaluate the first call in ... within data.table groups. See details for more information.

moreArgs list() A named list where each item is an argument one of the calls in ... which is not a column in the table being aggregated. Use to further parameterize you calls. Please note that these are not added to your aggregate calls unless you specify the names in the call.

Details

Use of Non-Standard Evaluation:
Arguments in ... are substituted and wrapped in a list, which is passed through to the j argument of [.data.table internally. The function currently tries to build informative column names for unnamed arguments in ... by appending the name of each function call with the name of its first argument, which is assumed to be the column name being aggregated over. If an argument to ... is named, that will be the column name of its value in the resulting data.table.

Enlisting:
The primary use case for enlist=FALSE is to allow computation of dependent aggregations, where the output from a previous aggregation is required in a subsequent one. For this case, wrap your call in { and assign intermediate results to variables, returning the final results as a list where each list item will become a column in the final table with the corresponding name. Name inference is disabled for this case, since it is assumed you will name the returned list items appropriately. A major advantage over multiple calls to aggregate is that the overhead of parallelization is paid only once even for complex multi-step computations like fitting a model, capturing its parameters, and making predictions using it. It also allows capturing arbitrarily complex calls which can be recomputed later using the update,TreatmentResponseExperiment-method. A potential disadvantage is increased RAM usage per thread due to storing intermediate values in variables, as well as any memory allocation overhead associate therewith.
**Value**

data.table of aggregation results.

**See Also**
data.table::[.data.table, BiocParallel::bplapply

---

**aggregate2**

Functional API for data.table aggregation which allows capture of associated aggregate calls so they can be recomputed later.

**Description**

Functional API for data.table aggregation which allows capture of associated aggregate calls so they can be recomputed later.

**Usage**

```r
aggregate2(
  x,
  by,
  ..., 
  nthread = 1,
  progress = interactive(),
  BPPARAM = NULL,
  enlist = TRUE,
  moreArgs = list()
)
```

**Arguments**

- `x` data.table
- `by` character One or more valid column names in x to compute groups using.
- `...` call One or more aggregations to compute for each group by in x. If you name aggregation calls, that will be the column name of the value in the resulting data.table otherwise a default name will be parsed from the function name and its first argument, which is assumed to be the name of the column being aggregated over.
- `nthread` numeric(1) Number of threads to use for split-apply-combine parallelization. Uses BiocParallel::bplapply if nthread > 1 or you pass in BPPARAM. Does not modify data.table threads, so be sure to use setDTthreads for reasonable nested parallelism. See details for performance considerations.
- `progress` logical(1) Display a progress bar for parallelized computations? Only works if bpprogressbar<- is defined for the current BiocParallel back-end.
BPPARAM

BiocParallelParam object. Use to customize the the parallelization back-end of bplapply. Note, nthread over-rides any settings from BPPARAM as long as bpworkers<~ is defined for that class.

enlist

logical(1) Default is TRUE. Set to FALSE to evaluate the first call in ... within data.table groups. See details for more information.

moreArgs

list() A named list where each item is an argument one of the calls in ... which is not a column in the table being aggregated. Use to further parameterize you calls. Please note that these are not added to your aggregate calls unless you specify the names in the call.

Details

Use of Non-Standard Evaluation:

Arguments in ... are substituted and wrapped in a list, which is passed through to the j argument of [.data.table internally. The function currently tries to build informative column names for unnamed arguments in ... by appending the name of each function call with the name of its first argument, which is assumed to be the column name being aggregated over. If an argument to ... is named, that will be the column name of its value in the resulting data.table.

Enlisting:

The primary use case for enlist=FALSE is to allow computation of dependent aggregations, where the output from a previous aggregation is required in a subsequent one. For this case, wrap your call in { and assign intermediate results to variables, returning the final results as a list where each list item will become a column in the final table with the corresponding name. Name inference is disabled for this case, since it is assumed you will name the returned list items appropriately. A major advantage over multiple calls to aggregate is that the overhead of parallelization is paid only once even for complex multi-step computations like fitting a model, capturing its parameters, and making predictions using it. It also allows capturing arbitrarily complex calls which can be recomputed later using the update,TreatmentResponseExperiment-method A potential disad-vantage is increased RAM usage per thread due to storing intermediate values in variables, as well as any memory allocation overhead associate therewith.

Value

data.table of aggregation results.

See Also

data.table::[.data.table, BiocParallel::bplapply

amcc

Calculate an Adaptive Matthews Correlation Coefficient
Description

This function calculates an Adaptive Matthews Correlation Coefficient (AMCC) for two vectors of values of the same length. It assumes the entries in the two vectors are paired. The Adaptive Matthews Correlation Coefficient for two vectors of values is defined as the Maximum Matthews Coefficient over all possible binary splits of the ranks of the two vectors. In this way, it calculates the best possible agreement of a binary classifier on the two vectors of data. If the AMCC is low, then it is impossible to find any binary classification of the two vectors with a high degree of concordance.

Usage

amcc(x, y, step.prct = 0, min.cat = 3, nperm = 1000, nthread = 1, ...)

Arguments

x, y Two paired vectors of values. Could be replicates of observations for the same experiments for example.
step.prct Instead of testing all possible splits of the data, it is possible to test steps of a percentage size of the total number of ranks in x/y. If this variable is 0, function defaults to testing all possible splits.
min.cat The minimum number of members per category. Classifications with less members fitting into both categories will not be considered.
nperm The number of permutation to use for estimating significance. If 0, then no p-value is calculated.
nthread Number of threads to parallize over. Both the AMCC calculation and the permutation testing is done in parallel.
... Additional arguments

Value

Returns a list with two elements. Samcc contains the highest 'mcc' value over all the splits, the p value, as well as the rank at which the split was done.

Examples

x <- c(1,2,3,4,5,6,7)
y <- c(1,3,5,4,2,7,6)
amcc(x,y, min.cat=2)
Coerce a LongTable to a TreatmentResponseExperiment

Description

Coerce a LongTable into a data.table. Currently only supports coercing to data.table or data.frame. Coerce a data.table with the proper configuration attributes back to a LongTable.

Arguments

from  A LongTableDataMapper to coerce.

Value

The data in object, as the child-class TreatmentResponseExperiment. A data.table with the data from a LongTable. data.table containing the data from the LongTable, with the ‘longTableDataMapper’ attribute containing the metadata needed to reverse the coercing operation. LongTable object configured with the longTableDataMapper data.table with long format of data in from data.frame with long format of data in from. SummarizedExperiment with each assay as a BumpyMatrix A TREDatamapper object.

See Also

TreatmentResponseExperiment BumpyMatrix::BumpyMatrix

Examples

data(clevelandSmall_cSet) TRE <- as(treatmentResponse(clevelandSmall_cSet), "TreatmentResponseExperiment") TRE as(merckLongTable, 'data.table')

dataTable <- as(merckLongTable, 'data.table') print(attr(dataTable, 'longTableDataMapper')) # Method doesn't work without this as(dataTable, 'LongTable')

SE <- molecularProfilesSlot(clevelandSmall_cSet)[[1]] as(SE, 'data.table')
as.long.table

Coerce from data.table to LongTable

Description
Coerce a data.table with the proper configuration attributes back to a LongTable

Usage
as.long.table(x)

Arguments
x
A data.frame with the 'longTableDataMapper' attribute, containing three lists named assayCols, rowDataCols and colDataCols. This attribute is automatically created when coercing from a LongTable to a data.table.

Value
LongTable object configured with the longTableDataMapper

Examples
dataTable <- as(merckLongTable, 'data.table')
print(attr(dataTable, 'longTableDataMapper')) # Method doesn't work without this
as.long.table(dataTable)

assay,LongTableDataMapper,ANY-method

Extract the data for an assay from a LongTableDataMapper

Description
Extract the data for an assay from a LongTableDataMapper

Usage
## S4 method for signature 'LongTableDataMapper,ANY'
assay(x, i, withDimnames = TRUE)
assay,TREDataMapper,ANY-method

Extract the data for an assay from a TREDataMapper

Arguments

- **x**: LongTableDataMapper The object to retrieve assay data form according to the assayMap slot.
- **i**: character(1) Name of an assay in the assayMap slot of `x`.
- **withDimnames**: logical(1) For compatibility with `SummarizedExperiment::assay` generic. Not used.

Value

data.table Data for the specified assay extracted from the rawdata slot of `x`.

---

assay,TREDataMapper,ANY-method

Extract the data for an assay from a TREDataMapper

Description

Extract the data for an assay from a TREDataMapper

Usage

```r
## S4 method for signature 'TREDataMapper,ANY'
assay(x, i, withDimnames = TRUE)
```

Arguments

- **x**: TREDataMapper The object to retrieve assay data form according to the assayMap slot.
- **i**: character(1) Name of an assay in the assayMap slot of `x`.
- **withDimnames**: logical(1) For compatibility with `SummarizedExperiment::assay` generic. Not used.

Value

data.table Data for the specified assay extracted from the rawdata slot of `x`. 
**assayCols**

*Generic to access the assay columns of a rectangular object.*

**Description**

Generic to access the assay columns of a rectangular object.

**Usage**

`assayCols(object, ...)`

**Arguments**

- `object` S4 An object to get assay ids from.
- `...` Allow new arguments to this generic.

**Value**

Depends on the implemented method.

**Examples**

```r
print("Generics shouldn't need examples?")
```

---

**assayIndex**

*Retrieve and assayIndex*

**Description**

Retrieve and assayIndex

**Usage**

`assayIndex(x, ...)`

**Arguments**

- `x` An S4 object.
- `...` `pairlist` Allow definition of new parameters for implementations of this generic.

**Value**

An object representing the "assayIndex" of an S4 object.
assays, LongTableDataMapper-method

Examples

print("Generics shouldn't need examples")

assayKeys

Retrieve a set of assayKeys

Description

Retrieve a set of assayKeys

Usage

assayKeys(x, ...)

Arguments

x An S4 object.
... pairlist Allow definition of new parameters for implementations of this generic.

Value

An object representing the "assayKeys" of an S4 object.

Examples

print("Generics shouldn't need examples")

assays, LongTableDataMapper-method

Extract the data for all assays from a LongTableDataMapper

Description

Extract the data for all assays from a LongTableDataMapper

Usage

## S4 method for signature 'LongTableDataMapper'
assays(x, withDimnames = TRUE)
assays,TREDataMapper-method

Arguments

x LongTableDataMapper The object to retrieve assay data form according to the assayMap slot.

withDimNames logical(1) For compatibility with SummarizedExperiment::assay generic. Not used.

Value

list Data for all assays extracted from the rawdata slot of x as a list of data.tables, where the keys for each table are their id_columns.

assays,TREDataMapper-method

Extract the data for all assays from a TREDataMapper

Description

Extract the data for all assays from a TREDataMapper

Usage

## S4 method for signature 'TREDataMapper'
assays(x, withDimNames = TRUE)

Arguments

x TREDatamapper The object to retrieve assay data form according to the assayMap slot.

withDimnames logical(1) For compatibility with SummarizedExperiment::assay generic. Not used.

Value

list Data for all assays extracted from the rawdata slot of x as a list of data.tables, where the keys for each table are their id_columns.
assignment-immutable  Intercept assignment operations for "immutable" S3 objects.

Description
Prevents modification of objects labelled with the "immutable" S3-class by intercepting assignment during S3-method dispatch and returning an error.

Usage
\method{subset}{immutable}(object, ...) <- value
## S3 replacement method for class 'immutable'
object[...] <- value

## S3 replacement method for class 'immutable'
object[[...]] <- value

## S3 replacement method for class 'immutable'
object$... <- value

## S3 replacement method for class 'immutable'
names(x) <- value

## S3 replacement method for class 'immutable'
dimnames(x) <- value

\method{colnames}{immutable}(x) <- value
\method{rownames}{immutable}(x) <- value

Arguments
object, x  An R object inheriting from the "immutable" S3-class.
...  Catch subset arguments for various dimensions.
value  Not used.

Value
None, throws an error.

Examples
immutable_df <- immutable(data.frame(a=1:5, b=letters[1:5]))
# return immutable data.frame
immutable_df[1:4, ]
# return immutable vector
buildComboProfiles

Build an assay table with an S4 object.

Usage

buildComboProfiles(object, ...)

Arguments

object S4 An S4 object a list-like slot containing assays for the object.
...
Allow new arguments to be defined for this generic.

Value
data.table.

Examples

"This is a generic method!"

buildComboProfiles,LongTable-method

Build an assay table with selected assay profiles for drug combinations

Description

Build an assay table with selected assay profiles for drug combinations

Usage

## S4 method for signature 'LongTable'
builtComboProfiles(object, profiles)

Arguments

object LongTable or inheriting class containing curated drug combination data.
profiles character a vector of profile names, i.e., column names of assays.
Value

A data.table containing fields treatment1id, treatment1dose, treatment2id, treatment2dose, sampleid, which are used as keys to keep track of profiles, along with columns of selected profiles from their assays. Each *_1 is the monotherapy profile of treatment 1 in the combination, and the same rule applies to treatment 2.

Examples

```r
# Not run:
combo_profile_1 <- buildComboProfiles(tre, c("auc", "SCORE"))
combo_profile_2 <- buildComboProfiles(tre, c("HS", "EC50", "E_inf", "ZIP"))
```

## End(Not run)

---

Build a LongTable object

Description

Build a LongTable object

Usage

```r
buildLongTable(from, ...)
```

Arguments

- `from` What to build the LongTable from?
- `...` pairlist Allow definition of new parameters for implementations of this generic.

Value

Depends on the implemented method

Examples

```r
print("Generics shouldn't need examples?")
```
**Description**

LongTable Create a LongTable object from a single .csv file

**Usage**

```r
## S4 method for signature 'character'
buildLongTable(from, rowDataCols, colDataCols, assayCols)
```

**Arguments**

- `from` character Path to the .csv file containing the data and metadata from which to build the LongTable.
- `rowDataCols` list List with two character vectors, the first specifying one or more columns to be used as cell identifiers (e.g., cell-line name columns) and the second containing any additional metadata columns related to the cell identifiers.
- `colDataCols` list List with two character vectors, the first specifying one or more columns to be used as column identifiers (e.g., drug name columns) and the second containing any additional metadata columns related to the column identifiers.
- `assayCols` list A named list of character vectors specifying how to parse assay columns into a list of data.tables. Each list data.table will be named for the name of corresponding list item and contain the columns specified in the character vector of column names in each list item.

**Value**

A LongTable object containing one or more assays, indexed by rowID and colID.

---

**Description**

Create a LongTable object from a single data.table or data.frame object.

**Usage**

```r
## S4 method for signature 'data.frame'
buildLongTable(from, rowDataCols, colDataCols, assayCols)
```
Arguments

from character Path to the .csv file containing the data and metadata from which to build the LongTable.

rowDataCols list List with two character vectors, the first specifying one or more columns to be used as cell identifiers (e.g., cell-line name columns) and the second containing any additional metadata columns related to the cell identifiers. If you wish to rename any of these columns, assign the new names to their respective character vectors.

colDataCols list List with two character vectors, the first specifying one or more columns to be used as column identifiers (e.g., drug name columns) and the second containing any additional metadata columns related to the column identifiers. If you wish to rename any of these columns, assign the new names to their respective character vectors.

assayCols list A named list of character vectors specifying how to parse assay columns into a list of data.tables. Each list data.table will be named for the name of corresponding list item and contain the columns specified in the character vector of column names in each list item. If there are no names for assayCols, the assays will be numbered by instead.

Value

A LongTable object containing one or more assays, indexed by rowID and colID.

Description

Create a LongTable object from a list containing file paths, data.frames and data.tables.

Usage

## S4 method for signature 'list'
bUILDLongTable(from, rowDataCols, colDataCols, assayCols)

Arguments

from list A list containing any combination of character file paths, data.tables and data.frames which will be used to construct the LongTable.

rowDataCols list List with two character vectors, the first specifying one or more columns to be used as cell identifiers (e.g., cell-line name columns) and the second containing any additional metadata columns related to the cell identifiers.

colDataCols list List with two character vectors, the first specifying one or more columns to be used as column identifiers (e.g., drug name columns) and the second containing any additional metadata columns related to the column identifiers.
assayCols  
A named list of character vectors specifying how to parse assay columns into a list of data.tables. Each list data.table will be named for the name of corresponding list item and contain the columns specified in the character vector of column names in each list item.

Value

A LongTable object constructed with the data in from.

Examples

```r
## Not run:
assayList <- assays(merckLongTable, withDimnames=TRUE)
rowDataCols <- list(rowIDs(merckLongTable), rowMeta(merckLongTable))
colDataCols <- list(colIDs(merckLongTable), colMeta(merckLongTable))
assayCols <- assayCols(merckLongTable)
longTable <- buildLongTable(from=assayList, rowDataCols, colDataCols, assayCols)
## End(Not run)
```

---

### c.immutable

*Intercept concatenation for "immutable" class objects to return another "immutable" class object.*

Description

Ensures that `c` and `append` to an "immutable" class object return an immutable class object.

Usage

```r
## S3 method for class 'immutable'
c(x, ...)
```

Arguments

- `x`: An R object inheriting from the "immutable" S3-class
- `...`: Objects to concatenate to `x`.

Value

`x` with one or more values appended to it.
callingWaterfall

Drug sensitivity calling using waterfall plots

Description

1. Sensitivity calls were made using one of IC50, ActArea or Amax

Usage

callingWaterfall(
  x,
  type = c("IC50", "AUC", "AMAX"),
  intermediate.fold = c(4, 1.2, 1.2),
  cor.min.linear = 0.95,
  name = "Drug",
  plot = FALSE
)

Arguments

x What type of object does this take in?
type ic50: IC50 values in micro molar (positive values) actarea: Activity Area, that
is area under the drug activity curve (positive values) amax: Activity at max
concentration (positive values)
intermediate.fold vector of fold changes used to define the intermediate sensitivities for ic50,
actarea and amax respectively
cor.min.linear numeric The minimum linear correlation to require?
name character The name of the output to use in plot
plot boolean Whether to plot the results

Details

1. Sort log IC50s (or ActArea or Amax) of the samples to generate a “waterfall distribution”
2. Identify cutoff:

3.1 If the waterfall distribution is non-linear (pearson cc to the linear fit <=0.95), estimate the major
inflection point of the log IC50 curve as the point on the curve with the maximal distance to a line
drawn between the start and end points of the distribution.
3.2 If the waterfall distribution appears linear (pearson cc to the linear fit > 0.95), then use the
median IC50 instead.

1. Samples within a 4-fold IC50 (or within a 1.2-fold ActArea or 20% Amax difference) differ-
ence centered around this inflection point are classified as being “intermediate”, samples with
lower IC50s (or ActArea/Amax values) than this range are defined as sensitive, and those with
IC50s (or ActArea/Amax) higher than this range are called “insensitive”.
2. Require at least x sensitive and x insensitive samples after applying these criteria (x=5 in our
case).
checkColumnCardinality

Value

factor Containing the drug sensitivity status of each sample.

Examples

# Dummy example
1 + 1

checkColumnCardinality

Search a data.frame for 1:cardinality relationships between a group of columns (your identifiers) and all other columns.

Description

Search a data.frame for 1:cardinality relationships between a group of columns (your identifiers) and all other columns.

Usage

checkColumnCardinality(df, group, cardinality = 1, ...)

Arguments

df A data.frame to search for 1:cardinality mappings with the columns in group.
group A character vector of one or more column names to check the cardinality of other columns against.
cardinality The cardinality of to search for (i.e., 1:cardinality) relationships with the combination of columns in group. Defaults to 1 (i.e., 1:1 mappings).
... Fall through arguments to data.table::[]. For developer use. One use case is setting verbose=TRUE to diagnose slow data.table operations.

Value

A character vector with the names of the columns with cardinality of 1:cardinality with the columns listed in group.

Examples

df <- rawdata(exampleDataMapper)
checkColumnCardinality(df, group='treatmentid')
checkCsetStructure  A function to verify the structure of a CoreSet

Description

This function checks the structure of a PharamcoSet, ensuring that the correct annotations are in place and all the required slots are filled so that matching of samples and drugs can be properly done across different types of data and with other studies.

Usage

checkCsetStructure(object, plotDist = FALSE, result.dir = tempdir())

Arguments

- object: A CoreSet to be verified
- plotDist: Should the function also plot the distribution of molecular data?
- result.dir: The path to the directory for saving the plots as a string. Defaults to this R sessions tempdir().

Value

Prints out messages whenever describing the errors found in the structure of the cSet object passed in.

Examples

checkCsetStructure(clevelandSmall_cSet)

clevelandSmall_cSet  Cleaveland_mut RadioSet subsetted and cast as CoreSet

Description

This dataset is just a dummy object derived from the Cleveland_mut RadioSet in the RadioGx R package. It's contents should not be interpreted and it is only present to test the functions in this package and provide examples.

Usage

data(clevelandSmall_cSet)

Format

CoreSet object
References


Description

Convenience method to subset the colData out of the rawdata slot using the assigned colDataMap metadata.

Usage

## S4 method for signature 'LongTableDataMapper'
colData(x, key = TRUE)

Arguments

x
LongTableDataMapper object with valid data in the rawdata and colDataMap slots.

key
logical(1) Should the table be keyed according to the id_columns of the colDataMap slot? This will sort the table in memory. Default is TRUE.

Value

data.table The colData as specified in the colDataMap slot.

Description

Convenience method to subset the colData out of the rawdata slot using the assigned colDataMap metadata.

Usage

## S4 method for signature 'TREDataMapper'
colData(x, key = TRUE)
Arguments

x  TREDDataMapper object with valid data in the rawdata and colDataMap slots.
key  logical(1) Should the table be keyed according to the id_columns of the colDataMap slot? This will sort the table in memory. Default is TRUE.

Value

data.table The colData as specified in the colDataMap slot.

Examples

print("Generics shouldn't need examples?")
**collect_fn_params**

*Collects all function arguments other than the first into a single list parameter.*

**Description**

Useful for converting a regular function into a function amenable to optimization via stats::optim, which requires all free parameters be passed as a single vector `par`.

**Usage**

```r
collect_fn_params(fn)
```

**Arguments**

- `fn` *function* A non-primitive function to refactor such that the first argument becomes the second argument and all other parameters must be passed as a vector to the first argument of the new function via the `par` parameter.

**Details**

Takes a function of the form `f(x, ...)`, where `...` is any number of additional function parameters (but not literal `...`!) and parses it to a function of the form `f(par, x)` where `par` is a vector of values for `...` in the same order as the arguments appear in `fn`.

**Value**

*function* A new non-primitive function where the first argument is `par`, which takes a vector of parameters being optimized, and the second argument is the old first argument to `fn` (usually `x` since this is the independent variable to optimize the function over).

---

**colMeta**

*Generic to access the column identifiers for a rectangular object.*

**Description**

Generic to access the column identifiers for a rectangular object.

**Usage**

```r
colMeta(object, ...)
```

**Arguments**

- `object` *S4* An object to get column metadata columns from.
- `...` *ALLOW NEW ARGUMENTS TO THIS GENERIC*
connectivityScore

Value

Depends on implemented method.

Examples

```r
print("Generics shouldn't need examples?")
```

connectivityScore  
*Function computing connectivity scores between two signatures*

Description

A function for finding the connectivity between two signatures, using either the GSEA method based on the KS statistic, or the gwc method based on a weighted spearman statistic. The GSEA analysis is implemented in the piano package.

Usage

```r
connectivityScore(
  x,
  y,
  method = c("fgsea", "gwc"),
  nperm = 10000,
  nthread = 1,
  gwc.method = c("spearman", "pearson"),
  ...
)
```

Arguments

- **x**: A matrix with the first gene signature. In the case of GSEA the vector of values per gene for GSEA in which we are looking for an enrichment. In the case of gwc, this should be a matrix, with the per gene responses in the first column, and the significance values in the second.
- **y**: A matrix with the second signature. In the case of GSEA, this is the vector of up and down regulated genes we are looking for in our signature, with the direction being determined from the sign. In the case of gwc, this should be a matrix of identical size to `x`, once again with the per gene responses in the first column, and their significance in the second.
- **method**: character string identifying which method to use, out of 'fgsea' and 'gwc'
- **nperm**: numeric, how many permutations should be done to determine significance through permutation testing? The minimum is 100, default is 1e4.
- **nthread**: numeric, how many cores to run parallel processing on.
- **gwc.method**: character, should gwc use a weighted spearman or pearson statistic?
- **...**: Additional arguments passed down to gsea and gwc functions
CoreGx-deprecated

Value

numeric a numeric vector with the score and the p-value associated with it

References


Examples

xValue <- c(1,5,23,4,8,9,2,19,11,12,13)
xSig <- c(0.01, 0.001, .97, 0.01,0.01,0.28,0.7,0.01,0.01,0.01,0.01)
yValue <- c(1,5,10,4,8,19,22,19,11,12,13)
ySig <- c(0.01, 0.001, .97,0.01, 0.01,0.78,0.9,0.01,0.01,0.01,0.01)
xx <- cbind(xValue, xSig)
yy <- cbind(yValue, ySig)
rownames(xx) <- rownames(yy) <- c('1', '2', '3', '4', '5', '6', '7', '8', '9', '10', '11')
data.cor <- connectivityScore(xx, yy, method='gwc', gwc.method='spearman', nperm=300)

CoreGx-deprecated

List of deprecated or defunct methods in the CoreGx R package.

Description

List of deprecated or defunct methods in the CoreGx R package.

Details

deprecated:

CoreSet: The CoreSet constructor is being updated to have a new API. This API is currently available via the CoreSet2 constructor. In Bioconductor 3.16, the old constructor will be renamed CoreSet2 and the new constructor will be renamed CoreSet.

defunct:

buildLongTable: This function no longer works as building a LongTable or TreatmentResponseExperiment now uses a DataMapper and the metaConstruct method. See vignette("LongTable") for a detailed description of how to create a LongTable object.
CoreSet 

CoreSet constructor

Description

A constructor that simplifies the process of creating CoreSets, as well as creates empty objects for data not provided to the constructor. Only objects returned by this constructor are expected to work with the CoreSet methods.

Usage

CoreSet(
  name,
  molecularProfiles = list(),
  sample = data.frame(),
  sensitivityInfo = data.frame(),
  sensitivityRaw = array(dim = c(0, 0, 0)),
  sensitivityProfiles = matrix(),
  sensitivityN = matrix(nrow = 0, ncol = 0),
  perturbationN = array(NA, dim = c(0, 0, 0)),
  curationSample = data.frame(),
  curationTissue = data.frame(),
  curationTreatment = data.frame(),
  treatment = data.frame(),
  datasetType = c("sensitivity", "perturbation", "both"),
  verify = TRUE,
  ...
)

Arguments

name 
A character string detailing the name of the dataset

molecularProfiles 
A list of SummarizedExperiment objects containing molecular profiles for each molecular data type.

sample 
A data.frame containing the annotations for all the sample profiled in the data set, across all data types. Must contain the mandatory sampleid column which uniquely identifies each sample in the object.

sensitivityInfo 
A data.frame containing the information for the sensitivity experiments. Must contain a 'sampleid' column with unique identifiers to each sample, matching the sample object and a 'treatmentid' columns with unique indenifiers for each treatment, matching the treatment object.

sensitivityRaw 
A 3 Dimensional array containing the raw drug dose response data for the sensitivity experiments
sensitivityProfiles
  data.frame containing drug sensitivity profile statistics such as IC50 and AUC
sensitivityN, perturbationN
  A data.frame summarizing the available sensitivity/perturbation data
curationSample, curationTissue, curationTreatment
  A data.frame mapping the names for samples, tissues and treatments used in the data set to universal identifiers used between different CoreSet objects
treatment
  A data.frame containing annotations for all treatments profiled in the dataset. Must contain the mandatory treatmentId column which uniquely identifies each treatment in the object.
datasetType
  A character(1) string of 'sensitivity', 'preturbation', or 'both' detailing what type of data can be found in the CoreSet, for proper processing of the data
verify
  logical(1) Should the function verify the CoreSet and print out any errors it finds after construction?
... Catch and parse any renamed constructor arguments.

Details

WARNING::
Parameters to this function have been renamed!
  • cell is now sample
  • drug is now treatment

Value
An object of class CoreSet

Examples

data(clevelandSmall_cSet)
clevelandSmall_cSet
Usage

```r
## S4 method for signature 'CoreSet'
annotation(object)

## S4 replacement method for signature 'CoreSet,list'
annotation(object) <- value

## S4 method for signature 'CoreSet'
dateCreated(object)

## S4 replacement method for signature 'CoreSet,character'
dateCreated(object) <- value

## S4 method for signature 'CoreSet'
name(object)

## S4 replacement method for signature 'CoreSet'
name(object) <- value

## S4 method for signature 'CoreSet'
sampleInfo(object)

## S4 replacement method for signature 'CoreSet,data.frame'
sampleInfo(object) <- value

## S4 method for signature 'CoreSet'
sampleNames(object)

## S4 replacement method for signature 'CoreSet,character'
sampleNames(object) <- value

## S4 method for signature 'CoreSet'
treatmentInfo(object)

## S4 replacement method for signature 'CoreSet,data.frame'
treatmentInfo(object) <- value

## S4 method for signature 'CoreSet'
treatmentNames(object)

## S4 replacement method for signature 'CoreSet,character'
treatmentNames(object) <- value

## S4 method for signature 'CoreSet'
curation(object)

## S4 replacement method for signature 'CoreSet,list'
curation(object) <- value
```
```r
## S4 method for signature 'CoreSet'
datasetType(object)

## S4 replacement method for signature 'CoreSet,character'
datasetType(object) <- value

## S4 method for signature 'CoreSet'
molecularProfiles(object, mDataType, assay)

## S4 replacement method for signature 'CoreSet,character,character,matrix'
molecularProfiles(object, mDataType, assay) <- value

## S4 replacement method for signature 'CoreSet,character,missing,matrix'
molecularProfiles(object, mDataType, assay) <- value

## S4 replacement method for signature 'CoreSet,missing,missing,list_OR_MAE'
molecularProfiles(object, mDataType, assay) <- value

## S4 method for signature 'CoreSet'
featureInfo(object, mDataType)

## S4 replacement method for signature 'CoreSet,character,data.frame'
featureInfo(object, mDataType) <- value

## S4 method for signature 'CoreSet,character'
phenoInfo(object, mDataType)

## S4 replacement method for signature 'CoreSet,character,data.frame'
phenoInfo(object, mDataType) <- value

## S4 method for signature 'CoreSet,character'
fNames(object, mDataType)

## S4 replacement method for signature 'CoreSet,character,character'
fNames(object, mDataType) <- value

## S4 method for signature 'CoreSet'
mDataNames(object)

## S4 replacement method for signature 'CoreSet'
mDataNames(object) <- value

## S4 method for signature 'CoreSet'
molecularProfilesSlot(object)

## S4 replacement method for signature 'CoreSet,list_OR_MAE'
molecularProfilesSlot(object) <- value
```
## S4 method for signature 'CoreSet'
sensitivityInfo(object, dimension, ...)

## S4 replacement method for signature 'CoreSet,data.frame'
sensitivityInfo(object, dimension, ...) <- value

## S4 method for signature 'CoreSet'
sensitivityMeasures(object)

## S4 replacement method for signature 'CoreSet,character'
sensitivityMeasures(object) <- value

## S4 method for signature 'CoreSet'
sensitivityProfiles(object)

## S4 replacement method for signature 'CoreSet,data.frame'
sensitivityProfiles(object) <- value

## S4 method for signature 'CoreSet'
sensitivityRaw(object)

## S4 replacement method for signature 'CoreSet,array'
sensitivityRaw(object) <- value

## S4 method for signature 'CoreSet'
treatmentResponse(object)

## S4 replacement method for signature 'CoreSet,list_OR_LongTable'
treatmentResponse(object) <- value

## S4 method for signature 'CoreSet'
sensNumber(object)

## S4 replacement method for signature 'CoreSet,matrix'
sensNumber(object) <- value

## S4 method for signature 'CoreSet'
pertNumber(object)

## S4 replacement method for signature 'CoreSet,array'
pertNumber(object) <- value

### Arguments

- **object**  
  A CoreSet object.

- **value**  
  See details.

- **mDataType**  
  character(1) The name of a molecular datatype to access from the molecularProfiles
assay character(1) A valid assay name in the SummarizedExperiment of @molecularProfiles of a CoreSet object for data type mDataType.

dimension See details.
...

Details

@annotation:

annotation: A list of CoreSet annotations with items: 'name', the name of the object; 'dateCreated', date the object was created; 'sessionInfo', the sessionInfo() when the object was created; 'call', the R constructor call; and 'version', the object version.

annotation<-: Setter method for the annotation slot. Arguments:

  • value: a list of annotations to update the CoreSet with.

@dateCreated:

dateCreated: character(1) The date the CoreSet object was created, as returned by the date() function.

dateCreated<-: Update the 'dateCreated' item in the annotation slot of a CoreSet object. Arguments:

  • value: A character(1) vector, as returned by the date() function.

name: character(1) The name of the CoreSet, retrieved from the @annotation slot.

name<-: Update the @annotation$name value in a CoreSet object.

  • value: character(1) The name of the CoreSet object.

cellInfo: data.frame Metadata for all sample in a CoreSet object.

sampleInfo<-: assign updated sample annotations to the CoreSet object. Arguments:

  • value: a data.frame object.

sampleNames: character Retrieve the rownames of the data.frame in the sample slot from a CoreSet object.

sampleNames<-: assign new rownames to the sampleInfo data.frame for a CoreSet object. Arguments:

  • value: character vector of rownames for the sampleInfo(object) data.frame.

treatmentInfo: data.frame Metadata for all treatments in a CoreSet object. Arguments:

  • object: CoreSet An object to retrieve treatment metadata from.

treatmentInfo<-: CoreSet object with updated treatment metadata. object. Arguments:

  • object: CoreSet An object to set treatment metadata for.
  • value: data.frame A new table of treatment metadata for object.
treatmentNames: character Names for all treatments in a CoreSet object. Arguments:
  - object: CoreSet An object to retrieve treatment names from.

treatmentNames<-: CoreSet Object with updates treatment names. object. Arguments:
  - object: CoreSet An object to set treatment names from.
  - value: character A character vector of updated treatment names.

@curation:
curation: A list of curated mappings between identifiers in the CoreSet object and the original
data publication. Contains two data.frames, 'sample' with sample ids and 'tissue' with tissue
ids.
curation<-: Update the curation slot of a CoreSet object. Arguments:
  - value: A list of data.frames, one for each type of curated identifier. For a CoreSet object
the slot should contain tissue and sample id data.frames.

datasetType slot:
datasetType: character(1) The type treatment response in the sensitivity slot. Valid values are
'sensitivity', 'perturbation' or 'both'.
datasetType<-: Update the datasetType slot of a CoreSet object. Arguments:
  - value: A character(1) vector with one of 'sensitivity', 'perturbation' or 'both'

@molecularProfiles:
molecularProfiles: matrix() Retrieve an assay in a SummarizedExperiment from the molecularProfiles
slot of a CoreSet object with the specified mDataType. Valid mDataType arguments can be found
with mDataNames(object). Exclude mDataType and assay to access the entire slot. Arguments:
  - assay: Optional character(1) vector specifying an assay in the SummarizedExperiment of
the molecularProfiles slot of the CoreSet object for the specified mDataType. If excluded,
defaults to modifying the first assay in the SummarizedExperiment for the given mDataType.
molecularProfiles<-: Update an assay in a SummarizedExperiment from the molecularProfiles
slot of a CoreSet object with the specified mDataType. Valid mDataType arguments can be found
with mDataNames(object). Omit mDataType and assay to update the slot.
  - assay: Optional character(1) vector specifying an assay in the SummarizedExperiment of
the molecularProfiles slot of the CoreSet object for the specified mDataType. If excluded,
defaults to modifying the first assay in the SummarizedExperiment for the given mDataType.
  - value: A matrix of values to assign to the assay slot of the SummarizedExperiment for the
selected mDataType. The rownames and column names must match the associated SummarizedExperiment.

featureInfo: Retrieve a DataFrame of feature metadata for the specified mDataType from the
molecularProfiles slot of a CoreSet object. More specifically, retrieve the @rowData slot from
the SummarizedExperiment from the @molecularProfiles of a CoreSet object with the name
mDataType.

featureInfo<-: Update the featureInfo(object, mDataType) DataFrame with new feature meta-
data. Arguments:
• value: A data.frame or DataFrame with updated feature metadata for the specified molecular profile in the molecularProfiles slot of a CoreSet object.

**phenoInfo**: Return the @colData slot from the SummarizedExperiment of mDataType, containing sample-level metadata, from a CoreSet object.

**phenoInfo<-**: Update the @colData slot of the SummarizedExperiment of mDataType in the @molecularProfiles slot of a CoreSet object. This updates the sample-level metadata in-place.

• value: A data.frame or DataFrame object where rows are samples and columns are sample metadata.

**fNames**: character() The features names from the rowData slot of a SummarizedExperiment of mDataType within a CoreSet object.

**fNames**: Updates the rownames of the feature metadata (i.e., rowData) for a SummarizedExperiment of mDataType within a CoreSet object.

• value: character() A character vector of new features names for the rowData of the SummarizedExperiment of mDataType in the @molecularProfiles slot of a CoreSet object. Must be the same length as nrow(featureInfo(object, mDataType)), the number of rows in the feature metadata.

**mDataNames**: character Retrieve the names of the molecular data types available in the molecularProfiles slot of a CoreSet object. These are the options which can be used in the mDataType parameter of various molecularProfiles slot accessors methods.

**mDataNames**: Update the molecular data type names of the molecularProfiles slot of a CoreSet object. Arguments:

• value: character vector of molecular datatype names, with length equal to length(molecularProfilesSlot(object)), the length of the molecularProfiles slot.

**molecularProfilesSlot**: Return the contents of the @molecularProfiles slot of a CoreSet object. This will either be a list or MultiAssayExperiment of SummarizedExperiments.

**molecularProfilesSlot<-**: Update the contents of the @molecularProfiles slot of a CoreSet object. Arguments:

• value: A list or MultiAssayExperiment of SummarizedExperiments. The list and assays should be named for the molecular datatype in each SummarizedExperiment.

**@treatmentResponse**: 

**Arguments**: 

• dimension: Optional character(1) One of 'treatment', 'sample' or 'assay' to retrieve rowData, colData or the 'assay_metadata' assay from the CoreSet @sensitivity LongTable object, respectively. Ignored with warning if @treatmentResponse is not a LongTable object.

• ...: Additional arguments to the rowData or colData. LongTable methods. Only used if the sensitivity slot contains a LongTable object instead of a list and the dimension argument is specified.

**Methods**: 

**sensitivityInfo**: DataFrame or data.frame of sensitivity treatment combo by sample metadata for the CoreSet object. When the dimension parameter is used, it allows retrieval of the dimension specific metadata from the LongTable object in @treatmentResponse of a CoreSet object.
sensitivityInfo<-: Update the @treatmentResponse slot metadata for a CoreSet object. When used without the dimension argument is behaves similar to the old CoreSet implementation, where the @treatmentResponse slot contained a list with a $info data.frame item. When the dimension argument is used, more complicated assignments can occur where 'sample' modifies the @sensitivity LongTable colData, 'treatment' the rowData and 'assay' the 'assay_metadata' assay. Arguments:

- value: A data.frame of treatment response experiment metadata, documenting experiment level metadata (mapping to treatments and samples). If the @treatmentResponse slot doesn’t contain a LongTable and dimension is not specified, you can only modify existing columns as returned by sensitivityInfo(object).

sensitivityMeasures: Get the 'sensitivityMeasures' available in a CoreSet object. Each measure represents some summary of sample sensitivity to a given treatment, such as ic50, ec50, AUC, AAC, etc. The results are returned as a character vector with all available metrics for the PSet object.

sensitivityMeasures<-: Update the sensitivity measure in a CoreSet object. These values are the column names of the 'profiles' assay and represent various computed sensitivity metrics such as ic50, ec50, AUC, AAC, etc.

- value: A character vector of new sensitivity measure names, the then length of the character vector must match the number of columns of the 'profiles' assay, excluding metadata and key columns.

sensitivityProfiles: Return the sensitivity profile summaries from the sensitivity slot. This data.frame contains various sensitivity summary metrics, such as ic50, amax, EC50, aac, HS, etc as columns, with rows as treatment by sample experiments.

sensitivityProfiles<-: Update the sensitivity profile summaries the sensitivity slot. Arguments:

- value: A data.frame the same number of rows as as returned by sensitivityProfiles(object), but potentially modified columns, such as the computation of additional summary metrics.

sensitivityRaw: Access the raw sensitivity measurements for a CoreSet object. A 3D array where rows are experiment_ids, columns are doses and the third dimension is metric, either 'Dose' for the doses used or 'Viability' for the sample viability at that dose.

sensitivityRaw<-: Update the raw dose and viability data in a CoreSet.

- value: A 3D array object where rows are experiment_ids, columns are replicates and pages are c('Dose', 'Viability'), with the corresponding dose or viability measurement for that experiment_id and replicate.

sensNumber: Return a count of viability observations in a CoreSet object for each treatment-combo by sample combination.

sensNumber<-: Update the 'n' item, which holds a matrix with a count of treatment by sample-line experiment counts, in the list in @treatmentResponse slot of a CoreSet object. Will error when @sensitivity contains a LongTable object, since the counts are computed on the fly. Arguments:

- value: A matrix where rows are samples and columns are treatments, with a count of the number of experiments for each combination as the values.

pertNumber: array Summary of available perturbation experiments from in a CoreSet object. Returns a 3D array with the number of perturbation experiments per treatment and sample, and data type.
**pertNumber**<-. Update the @perturbation$n value in a CoreSet object, which stores a summary of the available perturbation experiments. Arguments:

- **value**: A new 3D array with the number of perturbation experiments per treatment and sample, and data type

**Value**

Accessors: See details.

Setters: An updated CoreSet object, returned invisibly.

**Examples**

```r
data(clevelandSmall_cSet)
## @annotation
annotation(clevelandSmall_cSet)
annotation(clevelandSmall_cSet) <- annotation(clevelandSmall_cSet)
dateCreated(clevelandSmall_cSet)
## dateCreated
dateCreated(clevelandSmall_cSet) <- date()
name(clevelandSmall_cSet)
nname(clevelandSmall_cSet) <- 'new_name'
sampleInfo(clevelandSmall_cSet) <- sampleInfo(clevelandSmall_cSet)
sampleNames(clevelandSmall_cSet)
sampleNames(clevelandSmall_cSet) <- sampleNames(clevelandSmall_cSet)
treatmentInfo(clevelandSmall_cSet)
treatmentInfo(clevelandSmall_cSet) <- treatmentInfo(clevelandSmall_cSet)
treatmentNames(clevelandSmall_cSet)
treatmentNames(clevelandSmall_cSet) <- treatmentNames(clevelandSmall_cSet)
## curation
curation(clevelandSmall_cSet)
curation(clevelandSmall_cSet) <- curation(clevelandSmall_cSet)
datasetType(clevelandSmall_cSet)
datasetType(clevelandSmall_cSet) <- 'both'
```
# No assay specified
molecularProfiles(clevelandSmall_cSet, 'rna') <- molecularProfiles(clevelandSmall_cSet, 'rna')

# Specific assay
molecularProfiles(clevelandSmall_cSet, 'rna', 'exprs') <-
molecularProfiles(clevelandSmall_cSet, 'rna', 'exprs')

# Replace the whole slot
molecularProfiles(clevelandSmall_cSet) <- molecularProfiles(clevelandSmall_cSet)

featureInfo(clevelandSmall_cSet, 'rna')

featureInfo(clevelandSmall_cSet, 'rna') <- featureInfo(clevelandSmall_cSet, 'rna')

phenoInfo(clevelandSmall_cSet, 'rna')

phenoInfo(clevelandSmall_cSet, 'rna') <- phenoInfo(clevelandSmall_cSet, 'rna')

fNames(clevelandSmall_cSet, 'rna')

fNames(clevelandSmall_cSet, 'rna') <- fNames(clevelandSmall_cSet, 'rna')

mDataNames(clevelandSmall_cSet)

mDataNames(clevelandSmall_cSet) <- mDataNames(clevelandSmall_cSet)

molecularProfilesSlot(clevelandSmall_cSet)

molecularProfilesSlot(clevelandSmall_cSet) <- molecularProfilesSlot(clevelandSmall_cSet)

sensitivityInfo(clevelandSmall_cSet)

sensitivityInfo(clevelandSmall_cSet) <- sensitivityInfo(clevelandSmall_cSet)

sensitivityMeasures(clevelandSmall_cSet) <- sensitivityMeasures(clevelandSmall_cSet)

sensitivityMeasures(clevelandSmall_cSet) <- sensitivityMeasures(clevelandSmall_cSet)

sensitivityProfiles(clevelandSmall_cSet)

sensitivityProfiles(clevelandSmall_cSet) <- sensitivityProfiles(clevelandSmall_cSet)

head(sensitivityRaw(clevelandSmall_cSet))

sensitivityRaw(clevelandSmall_cSet) <- sensitivityRaw(clevelandSmall_cSet)

treatmentResponse(clevelandSmall_cSet)

treatmentResponse(clevelandSmall_cSet) <- treatmentResponse(clevelandSmall_cSet)

sensNumber(clevelandSmall_cSet)
sensNumber(clevelandSmall_cSet) <- sensNumber(clevelandSmall_cSet)
pertNumber(clevelandSmall_cSet)
pertNumber(clevelandSmall_cSet) <- pertNumber(clevelandSmall_cSet)

CoreSet-class  CoreSet - A generic data container for molecular profiles and treatment response data

Description
CoreSet - A generic data container for molecular profiles and treatment response data

Details
The CoreSet (cSet) class was developed as a superclass for pSets in the PharmacoGx and RadioGx packages to contain the data generated in screens of cancer sample lines for their genetic profile and sensitivities to therapy (Pharmacological or Radiation). This class is meant to be a superclass which is contained within the PharmacoSet (pSet) and RadioSet (rSet) objects exported by PharmacoGx and RadioGx. The format of the data is similar for both pSets and rSets, allowing much of the code to be abstracted into the CoreSet super-class. However, the models involved with quantifying sampleular response to Pharmacological and Radiation therapy are widely different, and extension of the cSet class allows the packages to apply the correct model for the given data.

Slots
- annotation: See Slots section.
- molecularProfiles: See Slots section.
- sample: See Slots section.
- treatment: See Slots section.
- treatmentResponse: See Slots section.
- perturbation: See Slots section.
- curation: See Slots section.
- datasetType: See Slots section.

Slots
- annotation: A list of annotation data about the CoreSet, including the $name and the session information for how the object was created, detailing the exact versions of R and all the packages used.
- molecularProfiles: A list or MultiAssayExperiment containing CoreSet object.
- sample: A data.frame containing the annotations for all the samples profiled in the data set, across all molecular data types and treatment response experiments.
- **treatment**: A `data.frame` containing the annotations for all treatments in the dataset, including the mandatory 'treatmentid' column to uniquely identify each treatment.
- **treatmentResponse**: A list or `LongTable` containing all the data for the treatment response experiment, including $info, a `data.frame` containing the experimental info, $raw a 3D array containing raw data, $profiles, a `data.frame` containing sensitivity profiles statistics, and $n, a `data.frame` detailing the number of experiments for each sample-drug/radiationInfo pair.
- **perturbation**: list containing $n, a `data.frame` summarizing the available perturbation data. This slot is currently being deprecated.
- **curation**: list containing mappings for treatment, sample and tissue names used in the data set to universal identifiers used between different CoreSet objects.
- **datasetType**: character string of 'sensitivity', 'perturbation', or both detailing what type of data can be found in the CoreSet, for proper processing of the data.

See Also

`CoreSet-accessors`

---

**Description**

Documentation for utility methods for a CoreSet object, such as set operations like subset and intersect. See @details for information on different types of methods and their implementations.

**Usage**

```r
# S4 method for signature 'CoreSet'
subsetBySample(x, samples)

# S4 method for signature 'CoreSet'
subsetByTreatment(x, treatments)

# S4 method for signature 'CoreSet'
subsetByFeature(x, features, mDataTypes)
```

**Arguments**

- `x`: A CoreSet object.
- `samples`: character() vector of sample names. Must be valid rownames from `sampleInfo(x)`.
- `treatments`: character() vector of treatment names. Must be valid rownames from `treatmentInfo(x)`. This method does not work with CoreSet objects yet.
- `features`: character() vector of feature names. Must be valid feature names for a given `mDataTypes`.
- `mDataTypes`: character() One or more molecular data types to to subset features by. Must be valid rownames for the selected `SummarizedExperiment` `mDataTypes`.
Details

subset methods:
subsetBySample: Subset a CoreSet object by sample identifier.
  • value: a CoreSet object containing only samples.

subset methods:
subsetByTreatment: Subset a CoreSet object by treatment identifier.
  • value: a CoreSet object containing only treatments.

subset methods:
subsetByFeature: Subset a CoreSet object by molecular feature identifier.
  • value: a CoreSet object containing only features.

Value

See details.

Examples

data(clevelandSmall_cSet)

## subset methods
### subsetBySample
samples <- sampleInfo(clevelandSmall_cSet)$sampleid[seq_len(10)]
clevelandSmall_cSet_sub <- subsetBySample(clevelandSmall_cSet, samples)

## subset methods
### subsetByTreatment
#treatments <- treatmentInfo(clevelandSmall_cSet)$treatmentid[seq_len(10)]
#clevelandSmall_cSet_sub <- subsetByTreatment(clevelandSmall_cSet, treatments)

## subset methods
### subsetByFeature
features <- fNames(clevelandSmall_cSet, 'rna')[seq_len(5)]
clevelandSmall_cSet_sub <- subsetByFeature(clevelandSmall_cSet, features, 'rna')
CoreSet2

*Make a CoreSet with the updated class structure*

**Description**

New implementation of the CoreSet constructor to support MAE and TRE. This constructor will be swapped with the original CoreSet constructor as part of an overhaul of the CoreSet class structure.

**Usage**

```r
CoreSet2(
  name = "emptySet",
  treatment = data.frame(),
  sample = data.frame(),
  molecularProfiles = MultiAssayExperiment(),
  treatmentResponse = LongTable(),
  datasetType = "sensitivity",
  perturbation = list(n = array(dim = 3), info = "No perturbation data!"),
  curation = list(sample = data.frame(), treatment = data.frame())
)
```

**Arguments**

- `name`: A character(1) vector with the CoreSet objects name.
- `treatment`: A data.frame with treatment level metadata.
- `sample`: A data.frame with sample level metadata for the union of samples in `treatmentResponse` and `molecularProfiles`.
- `molecularProfiles`: A MultiAssayExperiment containing one SummarizedExperiment object for each molecular data type.
- `treatmentResponse`: A LongTable or LongTableDataMapper object containing all treatment response data associated with the CoreSet object.
- `datasetType`: A deprecated slot in a CoreSet object included for backwards compatibility. This may be removed in future releases.
- `perturbation`: A deprecated slot in a CoreSet object included for backwards compatibility. This may be removed in future releases.
- `curation`: A list(2) object with two items named treatment and sample with mappings from publication identifiers to standardized identifiers for both annotations, respectively.

**Value**

A CoreSet object storing standardized and curated treatment response and multiomic profile data associated with a given publication.
cosinePerm

Examples

```r
data(clevelandSmall_cSet)
clevelandSmall_cSet
```

---

**cosinePerm**  
Cosine Permutations

**Description**

Computes the cosine similarity and significance using permutation test. This function uses random numbers, to ensure reproducibility please call `set.seed()` before running the function.

**Usage**

```r
cosinePerm(
  x,  
  y, 
  nperm = 1000, 
  alternative = c("two.sided", "less", "greater"), 
  include.perm = FALSE, 
  nthread = 1, 
  ... 
)
```

**Arguments**

- **x**  
  factor is the factors for the first variable
- **y**  
  factor is the factors for the second variable
- **nperm**  
  integer is the number of permutations to compute the null distribution of MCC estimates
- **alternative**  
  string indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association. Options are 'two.sided', 'less', or 'greater'
- **include.perm**  
  boolean indicates whether the estimates for the null distribution should be returned. Default set to 'FALSE'
- **nthread**  
  integer is the number of threads to be used to perform the permutations in parallel
- **...**  
  A list of fallback parameters

**Value**

A list estimate of the cosine similarity, p-value and estimates after random permutations (null distribution) in `include.perm` is set to 'TRUE'
Examples

```r
x <- factor(c(1,2,1,2,1))
y <- factor(c(2,2,1,1,1))
cosinePerm(x, y)
```

Description

Documentation for the various setters and getters which allow manipulation of data in the slots of a DataMapper object.

Usage

```r
## S4 method for signature 'DataMapper'
rawdata(object)

## S4 replacement method for signature 'DataMapper,ANY'
rawdata(object) <- value
```

Arguments

- **object**: A DataMapper object to get or set data from.
- **value**: A list-like object to assign to the rawdata slot. Should be a data.frame or data.table with the current implementation.

Details

- **rawdata**: Get the raw data slot from a DataMapper object. Returns a list-like containing one or more raw data inputs to the DataMapper object.
- **rawdata**: Set the raw data slot from a DataMapper object. **value**: The list-like object to set for the rawdata slot. Note: this currently only supports data.frame or data.table objects.

Value

- **Accessors**: See details
- **Setters**: An update DataMapper object, returned invisibly.

See Also

Other DataMapper-accessors: LongTableDataMapper-accessors, TREDDataMapper-accessors
DataMapper-class

An S4 Class For Mapping from Raw Experimental Data to a Specific S4 Object

Description

This object will be used as a way to abstract away data preprocessing.

Slots

- rawdata: A list-like object containing one or more pieces of raw data that will be processed and mapped to the slots of an S4 object.
- metadata: A List of object level metadata.

drop_fn_params

Drop parameters from a function and replace them with constants inside the function body.

Description

Drop parameters from a function and replace them with constants inside the function body.

Usage

drop_fn_params(fn, args)

Arguments

- fn function A non-primitive function to remove parameters from (via base::formals(fn)).
- args list A list where names are the function arguments (parameters) to remove and the values are the appropriate value to replace the parameter with in the function body.

Value

function A new non-primitize function with the parameters named in args deleted and their values fixed with the values from args in the function body.
drugSensitivitySig

*Compute the correlation between a molecular feature and treatment response*

**Description**
Compute the correlation between a molecular feature and treatment response

**Usage**
drugSensitivitySig(object, ...)

**Arguments**
- **object**: An object inheriting from `CoreGx::CoreSet` class
- **...**: Allow definition of new arguments to this generic

**Value**
A 3D array of genes x drugs x metric

endoaggregate

*Perform aggregation over an S4 object, but return an object of the same class.*

**Description**
Perform aggregation over an S4 object, but return an object of the same class.

**Usage**
endoaggregate(x, ...)

**Arguments**
- **x**: An S4 object to endomorphically aggregate over.
- **...** (pairlist): Allow definition of new parameters for implementations of this generic.

**Value**
An object with the same class as x.

**Examples**
print("Generics shouldn't need examples?"))
Description

Compute a group-by operation over a LongTable object or its inhering classes.

Usage

```r
## S4 method for signature 'LongTable'
endoaggregate(
  x,
  ...,
  assay,
  target = assay,
  by,
  subset = TRUE,
  nthread = 1,
  progress = TRUE,
  BPPARAM = NULL,
  enlist = TRUE,
  moreArgs = list()
)
```

Arguments

- **x**: LongTable or inhering class to compute aggregation on.
- **...**: call One or more aggregations to compute for each group by in x. If you name aggregation calls, that will be the column name of the value in the resulting data.table otherwise a default name will be parsed from the function name and its first argument, which is assumed to be the name of the column being aggregated over.
- **assay**: character(1) The assay to aggregate over.
- **target**: character(1) The assay to assign the results to. Defaults to assay.
- **by**: character One or more valid column names in x to compute groups using.
- **subset**: call An R call to evaluate before perfoming an aggregate. This allows you to aggregate over a subset of columns in an assay but have it be assigned to the parent object. Default is TRUE, which includes all rows. Passed through as the `i` argument in `[.data.table`.
- **nthread**: numeric(1) Number of threads to use for split-apply-combine parallelization. Uses BiocParallel::bplapply if nthread > 1 or you pass in BPPARAM. Does not modify data.table threads, so be sure to use setDTthreads for reasonable nested parallelism. See details for performance considerations.
**progress**

`logical(1)` Display a progress bar for parallelized computations? Only works if `bpprogressbar<-` is defined for the current BiocParallel back-end.

**BPPARAM**

`BiocParallelParam` object. Use to customized the the parallization back-end of `bplapply`. Note, `nthread` over-rides any settings from `BPPARAM` as long as `bpworkers<-` is defined for that class.

**enlist**

`logical(1)` Default is `TRUE`. Set to `FALSE` to evaluate the first call in `...` within `data.table` groups. See details for more information.

**moreArgs**

`list()` A named list where each item is an argument one of the calls in `...` which is not a column in the table being aggregated. Use to further parameterize your calls. Please note that these are not added to your aggregate calls unless you specify the names in the call.

## Details

### Use of Non-Standard Evaluation:

Arguments in `...` are substituted and wrapped in a list, which is passed through to the `j` argument of ` [.data.table` internally. The function currently tries to build informative column names for unnamed arguments in `...` by appending the name of each function call with the name of its first argument, which is assumed to be the column name being aggregated over. If an argument to `...` is named, that will be the column name of its value in the resulting `data.table`.

### Enlisting:

The primary use case for `enlist=FALSE` is to allow computation of dependent aggregations, where the output from a previous aggregation is required in a subsequent one. For this case, wrap your call in `(` and assign intermediate results to variables, returning the final results as a list where each list item will become a column in the final table with the corresponding name. Name inference is disabled for this case, since it is assumed you will name the returned list items appropriately. A major advantage over multiple calls to `aggregate` is that the overhead of parallelization is paid only once even for complex multi-step computations like fitting a model, capturing its parameters, and making predictions using it. It also allows capturing arbitrarily complex calls which can be recomputed later using the `update,TreatmentResponseExperiment-method` A potential disadvantage is increased RAM usage per thread due to storing intermediate values in variables, as well as any memory allocation overhead associate therewith.

## Value

Object with the same class as `x`, with the aggregation results assigned to `target`, using `strategy` if `target` is an existing assay in `x`.

## See Also

`data.table::[.data.table, BiocParallel::bplapply`
**Example LongTableDataMapper**

**Description**

A dummy LongTableDataMapper object to be used in package examples.

**Usage**

```r
data(exampleDataMapper)
```

**Format**

LongTableDataMapper object

**getIntern**

*Retrieve the specified item from object internal metadata.*

**Description**

Internal slot for storing metadata relevant to the internal operation of an S4 object.

**Usage**

```r
getIntern(object, x, ...)
```

**Arguments**

- **object**
  - S4 An object with an `.intern` slot containing an environment.
- **x**
  - character One or more symbol names to retrieve from the object `.intern` environment.
- **...**
  - Allow new parameters to be defined for this generic.

**Details**

Warning: This method is intended for developer use and can be ignored by users.

**Value**

Depends on the implemented method

**Examples**

```r
print("Generics shouldn't need examples?")
```
getIntern<-  

Set the internal structural metadata for an S4 class

Description

Set the internal structural metadata for an S4 class

Usage

getIntern(object, ...) <- value

Arguments

- object: An R object to update internal structural metadata for.
- value: An immutable_list object, being a class union between list and immutable S3 classes.

Value

Updates the object and returns invisibly.

Examples

print("Generics shouldn’t need examples?")

getIntern<-,LongTable,immutable_list-method

Set the .intern slot of a LongTable

Description

Set the .intern slot of a LongTable

Usage

## S4 replacement method for signature 'LongTable,immutable_list'
getIntern(object) <- value

Arguments

- object: LongTable
- value: An immutable_list object, being a class union between list and immutable S3 classes.

Value

Updates the object and returns invisibly.
guessMapping

Generic for Guessing the Mapping Between Some Raw Data and an S4 Object

Description

Generic for Guessing the Mapping Between Some Raw Data and an S4 Object

Usage

guessMapping(object, ...)

Arguments

object An S4 object containing so raw data to guess data to object slot mappings for.
...
Allow new arguments to be defined for this generic.

Value

A list with mapping guesses as items.

Examples

"Generics shouldn't need examples!"

guessMapping,LongTableDataMapper-method

Guess which columns in raw experiment data map to which dimensions.

Description

Checks for columns which are uniquely identified by a group of identifiers. This should be used to help identify the columns required to uniquely identify the rows, columns, assays and metadata of a DataMapper class object.

Usage

## S4 method for signature 'LongTableDataMapper'
guessMapping(object, groups, subset, data = FALSE)
Arguments

object: A LongTableDataMapper object.

groups: A list containing one or more vector of column names to group-by. The function uses these to determine 1:1 mappings between the combination of columns in each vector and unique values in the raw data columns.

subset: A logical vector indicating whether to subset out mapped columns after each grouping. Must be a single TRUE or FALSE or have the same length as groups, indicating whether to subset out mapped columns after each grouping. This will prevent mapping a column to two different groups.

data: A logical vector indicating whether you would like the data for mapped columns to be returned instead of their column names. Defaults to FALSE for easy use assigning mapped columns to a DataMapper object.

Details

Any unmapped columns will be added to the end of the returned list in an item called unmapped.

The function automatically guesses metadata by checking if any columns have only a single value. This is returned as an additional item in the list.

Value

A list, where each item is named for the associated groups item the guess is for. The character vector in each item are columns which are uniquely identified by the identifiers from that group.

Examples

guessMapping(exampleDataMapper, groups=list(rows='treatmentid', cols='sampleid'), subset=FALSE)

---

gwc

\textit{GWC Score}

Description

Calculate the gwc score between two vectors, using either a weighted spearman or pearson correlation

Usage

gwc(
x1,
p1,
x2,
p2,
method.cor = c("pearson", "spearman"),
 Arguments

  x1      numeric vector of effect sizes (e.g., fold change or t statistics) for the first experiment
  p1      numeric vector of p-values for each corresponding effect size for the first experiment
  x2      numeric effect size (e.g., fold change or t statistics) for the second experiment
  p2      numeric vector of p-values for each corresponding effect size for the second experiment
  method.cor character string identifying if a pearson or spearman correlation should be used
  nperm numeric how many permutations should be done to determine
  truncate.p numeric Truncation value for extremely low p-values
...    Other passed down to internal functions

 Value

 numeric a vector of two values, the correlation and associated p-value.

 Examples

    data(clevelandSmall_cSet)
    x <- molecularProfiles(clevelandSmall_cSet,'rna')[,1]
    y <- molecularProfiles(clevelandSmall_cSet,'rna')[,2]
    x_p <- rep(0.05, times=length(x))
    y_p <- rep(0.05, times=length(y))
    names(x_p) <- names(x)
    names(y_p) <- names(y)
    gwc(x,x_p,y,y_p, nperm=100)
Arguments

- object: An S4 object to get id columns from.
- ...: Allow new arguments to this generic.

Value

Depends on the implemented method

Examples

print("Generics shouldn't need examples?")

---

**immutable**

Constructor for "immutable" S3-class property

Description

This method should allow any S3 object in R to become immutable by intercepting `[<-`, `[[<-`, `$<-` and `c` during S3-method dispatch and returning an error.

Reverse with call to the mutable function.

Usage

immutable(object)

is.immutable(object)

## S3 method for class 'immutable'

print(x, ...)

show.immutable(x)

Arguments

- object, x: Any R object which uses S3 method dispatch
- ...: Fallthrough arguments to `print.default`.

Details

The motivation for this class was to create pseudo-private slots in an R S4 object by preventing mutation of those slots outside of the accessors written for the class. It should behave as expected for R object which operate with 'copy-on-modify' semantics, including most base R functions and S3 objects.

An environment was not suitable for this case due to the 'copy-by-reference' semantics, such that normal R assignment, which users assume makes a copy of the object, actually references the same environment in both the original and copy of the object.
is.items

WARNING: This implementation is unable to intercept modifications to a data.table via the set* group of methods. This is because these methods are not S3 generics and therefore no mechanism exists for hooking into them to extend their functionality. In general, this helper class will only work for objects with an S3 interface.

Value
The object with "immutable" prepended to its class attribute.

logical(1) Does the object inherit from the "immutable" S3-class?
None, invisible(NULL)

See Also
assignment-immutable, setOps-immutable

Examples

immutable_list <- immutable(as.list(1:5))
class(immutable_list)
# errors during assignment operations
tryCatch({ immutable_list$new <- 1 }, error=print)

is.immutable(immutable_list)

is.items(list, ..., FUN = is)

Description
Get the types of all items in a list

Usage

is.items(list, ..., FUN = is)

Arguments

list A list to get the types from
... pairlist Additional arguments to FUN
FUN function or character Either a function, or the name of a function which returns a single logical value. The default function uses is, specify the desired type in .... You can also use other type checking functions such as is.character, is.numeric, or is.data.frame.
lapply,MultiAssayExperiment-method

Value

logical A vector indicating if the list item is the specified type.

Examples

list <- list(c(1,2,3), c('a','b','c'))
is.items(list, 'character')

is_optim_compatible

Check whether a function signature is amenable to optimization via
stats::optim.

Description

Functions compatible with optim have the parameter named par as their first formal argument
where each value is a respective free parameter to be optimized.

Usage

is_optim_compatible(fn)

Arguments

fn function A non-primitive function.

Value

logical(1) TRUE if the first value of formalArg(fn) is "par", otherwise FALSE.

lapply,MultiAssayExperiment-method

lapply lapply method for MultiAssayExperiment

Description

lapply lapply method for MultiAssayExperiment

Usage

## S4 method for signature 'MultiAssayExperiment'
lapply(X, FUN, ...)
Arguments

X 
A MultiAssayExperiment object.

FUN 
A function to be applied to each SummarizedExperiment in a in X.

... 
Fall through parameters to FUN

Value

A MultiAssayExperiment object, modified such that experiments(X) <- endoapply(experiments(X), FUN, ...).s

Description

A class union to allow multiple types in a CoreSet slot

LongTable

LongTable constructor method

Description

LongTable constructor method

Usage

LongTable(
  rowData,
  rowIDs,
  colData,
  colIDs,
  assays,
  assayIDs,
  metadata = list(),
  keep.rownames = FALSE
)
### Arguments

- **rowData** data.frame A rectangular object coercible to a data.table.
- **rowIDs** character A vector of rowData column names needed to uniquely identify each row in a LongTable.
- **colData** data.frame A rectangular object coercible to a data.table.
- **colIDs** character A vector of colData column names needed to uniquely identify each column in a LongTable.
- **assays** list A list of rectangular objects, each coercible to a data.table. Must be named and item names must match the assayIDs list.
- **assayIDs** list A list of character vectors specifying the columns needed to uniquely identify each row in an assay. Names must match the assays list.
- **metadata** list A list of one or more metadata items associated with a LongTable experiment.
- **keep.rownames** logical(1) or character(1) Should rownames be retained when coercing to data.table inside the constructor. Default is FALSE. If TRUE, adds a 'rn' column to each rectangular object that gets coerced from data.frame to data.table. If a string, that becomes the name of the rownames column.

### Value

A LongTable object containing the data for a treatment response experiment and configured according to the rowIDs and colIDs arguments.

### Examples

"See vignette('The LongTable Class', package='CoreGx')"
LongTable-class

LongTable class definition

Description

Define a private constructor method to be used to build a LongTable object.
This is used as an alternative to R attributes for storing structural metadata of an S4 objects.
Add or replace an assay in a LongTable by name. Currently this function only works when the assay
has all columns in row and column data tables (i.e., when assays is returned with Dimnames=TRUE).
Select an assay from within a LongTable object.

Usage

```r
## S4 method for signature 'LongTable'
rowIDs(object, data = FALSE, key = FALSE)

## S4 method for signature 'LongTable'
rowMeta(object, data = FALSE, key = FALSE)

## S4 method for signature 'LongTable'
colIDs(object, data = FALSE, key = FALSE)

## S4 method for signature 'LongTable'
colMeta(object, data = FALSE, key = FALSE)

## S4 method for signature 'LongTable'
idCols(object)

## S4 method for signature 'LongTable'
assayIndex(x)

## S4 method for signature 'LongTable'
assayKeys(x, i)

## S4 method for signature 'LongTable'
assayCols(object, i)

## S4 method for signature 'LongTable,character'
getIntern(object, x)

## S4 method for signature 'LongTable,missing'
getIntern(object, x)

## S4 method for signature 'LongTable'
rowData(x, key = FALSE, use.names = FALSE, ...)
```
## S4 replacement method for signature 'LongTable'
rowData(x, ...) <- value

## S4 method for signature 'LongTable'
colData(x, key = FALSE, dimnames = FALSE, ...)

## S4 replacement method for signature 'LongTable,ANY'
colData(x, ...) <- value

## S4 method for signature 'LongTable'
assays(
  x,
  withDimnames = TRUE,
  metadata = withDimnames,
  key = !withDimnames,
  ...
)

## S4 replacement method for signature 'LongTable,list'
assays(x, withDimnames = TRUE, ...) <- value

## S4 method for signature 'LongTable,ANY'
assay(
  x,
  i,
  withDimnames = TRUE,
  summarize = withDimnames,
  metadata = !summarize,
  key = !(summarize || withDimnames),
  ...
)

## S4 replacement method for signature 'LongTable,ANY'
assay(x, i) <- value

## S4 method for signature 'LongTable'
assayNames(x)

## S4 method for signature 'LongTable,ANY,ANY'
x[[i]]

## S4 method for signature 'LongTable'
dim(x)

## S4 method for signature 'LongTable'
colnames(x)

## S4 method for signature 'LongTable'
LongTable-class

rownames(x)
## S4 method for signature 'LongTable'
dimnames(x)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>LongTable</td>
</tr>
<tr>
<td>data</td>
<td>logical</td>
</tr>
<tr>
<td>key</td>
<td>logical</td>
</tr>
<tr>
<td>x</td>
<td>The LongTable object to retrieve the dimnames for.</td>
</tr>
<tr>
<td>i</td>
<td>character(1) name or integer index of the desired assay.</td>
</tr>
<tr>
<td>use.names</td>
<td>logical</td>
</tr>
<tr>
<td>...</td>
<td>For developer use only! Pass raw=TRUE to return the slot for modification by reference.</td>
</tr>
<tr>
<td>value</td>
<td>A data.frame or data.table to update the assay data with. This must at minimum contain the row and column data identifier columns to allow correctly mapping the assay keys. We recommend modifying the results returned by assay(LongTable, 'assayName', withDimnames=TRUE). For convenience, both the [[ and $ LongTable accessors return an assay with the dimnames.</td>
</tr>
<tr>
<td>withDimnames</td>
<td>logical(1)</td>
</tr>
<tr>
<td>metadata</td>
<td>logical(1)</td>
</tr>
<tr>
<td>summarize</td>
<td>logical(1)</td>
</tr>
<tr>
<td>'x'</td>
<td>A LongTable or inheriting class.</td>
</tr>
<tr>
<td>'i'</td>
<td>An optional valid assay name or index in x.</td>
</tr>
</tbody>
</table>

Value

LongTable object containing the assay data from a treatment response experiment

A character vector of rowData column names if data is FALSE, otherwise a data.table with the data from the rowData id columns.

A character vector of rowData column names if data is FALSE, otherwise a data.table with the data from the rowData metadata columns.
A character vector of colData column names if data is FALSE, otherwise a data.table with the data from the colData id columns.

A character vector of colData column names if data is FALSE, otherwise a data.table with the data from the colData metadata columns.

character A character vector containing the unique rowIDs and colIDs in a LongTable object.

A mutable copy of the "assayIndex" for x

A mutable copy of the "assyKeys" for x

A list of character vectors containing the value column names for each assay if i is missing, otherwise a character vector of value column names for the selected assay.

immutable value of x if length(x) == 1 else named list of values for all symbols in x.

An immutable list.

A data.table containing rowID, row identifiers, and row metadata.

A copy of the LongTable object with the rowData slot updated.

A data.table containing row identifiers and metadata.

A copy of the LongTable object with the colData slot updated.

A list of data.table objects, one per assay in the object.

A copy of the LongTable with the assays modified.

LongTable With updated assays slot.

character Names of the assays contained in the LongTable.

numeric Vector of object dimensions.

character Vector of column names.

character Vector of row names.

list List with two character vectors, one for row and one for column names.

Methods (by generic)

- rowMeta(LongTable): Get the names of the non-id columns from rowData.
- colIDs(LongTable): Get the names of the columns in colData required to uniquely identify each row.
- colMeta(LongTable): Get the names of the non-id columns in the colData data.table.
- idCols(LongTable): Get the names of all id columns.
- assayIndex(LongTable): Get the assayIndex item from the objects internal metadata.
- assayKeys(LongTable): Get the assayKeys item from the objects internal metadata.
- assayCols(LongTable): Get a list of column names for each assay in the object.
- getIntern(object = LongTable, x = character): Access structural metadata present within a LongTable object. This is mostly for developer use.
- getIntern(object = LongTable, x = missing): Access all structural metadata present within a LongTable object. This is primarily for developer use.
- rowData(LongTable): Get the row level annotations for a LongTable object.
LongTable-class

- `rowData(LongTable) <- value`: Update the row annotations for a LongTable object. Currently requires that all columns in rowIDs(longTable) be present in value.
- `colData(LongTable)`: Get the column level annotations for a LongTable object.
- `colData(x = LongTable) <- value`: Update the colData of a LongTable object. Currently requires that all of the colIDs(longTable) be in the value object.
- `assays(LongTable)`: Get a list containing all the assays in a LongTable.
- `assays(x = LongTable) <- value`: Update the assays in a LongTable object. The rowIDs and colIDs must be present in all assays to allow successfully remapping the keys. We recommend modifying the list returned by assays(longTable, withDimnames=TRUE) and the reassigning to the LongTable.
- `assay(x = LongTable, i = ANY)`: Retrieve an assay data.table object from the assays slot of a LongTable object.
- `assay(x = LongTable, i = ANY) <- value`:
- `assayNames(LongTable)`: Return the names of the assays contained in a LongTable
- `x[i]`: Get an assay from a LongTable object. This method returns the row and column annotations by default to make assignment and aggregate operations easier.
- `dim(LongTable)`: Get the number of row annotations by the number of column annotations from a LongTable object. Please note that row x columns does not necessarily equal the number of rows in an assay, since it is not required for each assay to have every row or column present.
- `colnames(LongTable)`: Retrieve the pseudo-colnames of a LongTable object, these are constructed by pasting together the colIDs(longTable) and can be used in the subset method for regex based queries.
- `rownames(LongTable)`: Retrieve the pseudo-rownames of a LongTable object, these are constructed by pasting together the rowIDs(longTable) and can be used in the subset method for regex based queries.
- `dimnames(LongTable)`: Get the pseudo-dimnames for a LongTable object. See colnames and rownames for more information.

### Slots

- `rowData` See Slots section.
- `colData` See Slots section.
- `assays` See Slots section.
- `metadata` See Slots section.
- `.intern` See Slots section.

### Slots

- `rowData`: A data.table containing the metadata associated with the row dimension of a LongTable.
- `colData`: A data.table containing the metadata associated with the column dimension of a LongTable.
• **assays:** A list of data.tables, one for each assay in a LongTable.

• **metadata:** An optional list of additional metadata for a LongTable which doesn’t map to one of the dimensions.

• **.intern:** An immutable list that holds internal structural metadata about a LongTable object, such as which columns are required to key the object.

**Examples**

```r
colIDs(merckLongTable)
rowIDs(merckLongTable)
colMeta(merckLongTable)
rowMeta(merckLongTable)
idCols(merckLongTable)
assayIndex(nci_TRE_small)
assayKeys(nci_TRE_small)
assayKeys(nci_TRE_small, "sensitivity")
assayKeys(nci_TRE_small, 1)
assayCols(merckLongTable)
getIntern(merckLongTable, 'rowIDs')
getIntern(merckLongTable, c('colIDs', 'colMeta'))
rowData(merckLongTable)
rowData(merckLongTable) <- rowData(merckLongTable)
colData(merckLongTable)

# Get the keys as well, mostly for internal use
colData(merckLongTable, key=TRUE)

colData(merckLongTable) <- colData(merckLongTable)
assays(merckLongTable)
assays(merckLongTable) <- assays(merckLongTable, withDimnames=TRUE)

# Default annotations, just the key columns
assay(merckLongTable, 'sensitivity')
assay(merckLongTable, 1)

# With identifiers joined
assay(merckLongTable, 'sensitivity', withDimnames=TRUE)
```
LongTableDataMapper

Constructor for the `LongTableDataMapper` class, which maps from one or more raw experimental data files to the slots of a `LongTable` object.

Description

Constructor for the `LongTableDataMapper` class, which maps from one or more raw experimental data files to the slots of a `LongTable` object.

Usage

```r
LongTableDataMapper(
  rawdata = data.frame(),
  rowDataMap = list(character(), character()),
  colDataMap = list(character(), character()),
  assayDataMap = list(list(character(), character())),
  metadataMap = list(character())
)
```

Arguments

- `rawdata` A `data.frame` of raw data from a treatment response experiment. This will be coerced to a `data.table` internally. We recommend using joins to aggregate your raw data if it is not present in a single file.
**rowDataMap**  A list-like object containing two character vectors. The first is column names in `rawdata` needed to uniquely identify each row, the second is additional columns which map to rows, but are not required to uniquely identify them. Rows should be drugs.

**colDataMap**  A list-like object containing two character vectors. The first is column names in `rawdata` needed to uniquely identify each column, the second is additional columns which map to rows, but are not required to uniquely identify them. Columns should be samples.

**assayMap**  A list-like where each item is a list with two character vectors defining an assay, the first containing the identifier columns in `rawdata` needed to uniquely identify each row an assay, and the second the `rawdata` columns to be mapped to that assay. The names of `assayMap` will be the names of the assays in the `LongTable` that is created when calling `metaConstruct` on this `DataMapper` object. If the character vectors have names, the value columns will be renamed accordingly.

**metadataMap**  A list-like where each item is a character vector of `rawdata` column names to assign to the `@metadata` of the `LongTable`, where the name of that assay is the name of the list item. If names are omitted, assays will be numbered by their index in the list.

**Details**

The `guessMapping` method can be used to test hypotheses about the cardinality of one or more sets of identifier columns. This is helpful to determine the id columns for `rowDataMap` and `colDataMap`, as well as identify columns mapping to assays or metadata.

To attach metadata not associated with `rawdata`, please use the metadata assignment method on your `LongTableDataMapper`. This metadata will be merged with any metadata from `metadataMap` and added to the `LongTable` which this object ultimately constructs.

**Value**

A `LongTable` object, with columns mapped to it’s slots according to the various maps in the `LongTableDataMapper` object.

**See Also**

`guessMapping`

**Examples**

data(exampleDataMapper)
exampleDataMapper
Description

Documentation for the various setters and getters which allow manipulation of data in the slots of a LongTableDataMapper object.

Usage

```r
## S4 replacement method for signature 'LongTableDataMapper,list'
rawdata(object) <- value

## S4 method for signature 'LongTableDataMapper'
rowDataMap(object)

## S4 replacement method for signature 'LongTableDataMapper,list_OR_List'
rowDataMap(object) <- value

## S4 method for signature 'LongTableDataMapper'
colDataMap(object)

## S4 replacement method for signature 'LongTableDataMapper,list_OR_List'
colDataMap(object) <- value

## S4 method for signature 'LongTableDataMapper'
assayMap(object)

## S4 replacement method for signature 'LongTableDataMapper,list_OR_List'
assayMap(object) <- value

## S4 method for signature 'LongTableDataMapper'
metadataMap(object)

## S4 replacement method for signature 'LongTableDataMapper,list_OR_List'
metadataMap(object) <- value
```

Arguments

- **object**: A LongTableDataMapper object to get or set data from.
- **value**: See details.

Details

- **rawdata**: Get the raw data slot from a LongTableDataMapper object. Returns a list-like containing one or more raw data inputs to the LongTableDataMapper object.
**rawdata**: Set the raw data slot from a `LongTableDataMapper` object. **value**: The list-like object to set for the rawdata slot. Note: this currently only supports `data.frame` or `data.table` objects.

**rowDataMap**: list of two character vectors, the first are the columns required to uniquely identify each row of a `LongTableDataMapper` and the second any additional row-level metadata. If the character vectors have names, the resulting columns are automatically renamed to the item name of the specified column.

**rowDataMap**: Update the @rowDataMap slot of a `LongTableDataMapper` object, returning an invisible NULL. Args:
- `value`: A list or `List` where the first item is the names of the identifier columns – columns needed to uniquely identify each row in rowData – and the second item is the metadata associated with those the identifier columns, but not required to uniquely identify rows in the object rowData.

**colDataMap**: list of two character vectors, the first are the columns required to uniquely identify each row of a `LongTableDataMapper` and the second any additional col-level metadata. If the character vectors have names, the resulting columns are automatically renamed to the item name of the specified column.

**colDataMap**: Update the @colDataMap slot of a `LongTableDataMapper` object, returning an invisible NULL. Args:
- `value`: A list or `List` where the first item is the names of the identifier columns – columns needed to uniquely identify each row in colData – and the second item is the metadata associated with those the identifier columns, but not required to uniquely identify rows in the object rowData.

**assayMap**: A list of character vectors. The name of each list item will be the assay in a `LongTableDataMapper` object that the columns in the character vector will be assigned to. Column renaming occurs automatically when the character vectors have names (from the value to the name).

**assayMap**: Updates the @assayMap slot of a `LongTableDataMapper` object, returning an invisible NULL. Args:
- `value`: A list of character vectors, where the name of each list item is the name of an assay and the values of each character vector specify the columns mapping to the assay in the S4 object the `LongTableDataMapper` constructs.

**metadataMap**: A list of character vectors. Each item is an element of the constructed objects @metadata slot.

**metadataMap**: Updates `LongTableDataMapper` object in-place, then returns an invisible(NULL). Args:
- `value`: A list of character vectors. The name of each list item is the name of the item in the @metadata slot of the `LongTableDataMapper` object created when `metaConstruct` is called on the `DataMapper`, and a character vector specifies the columns of @rawdata to assign to each item.

**Value**

Accessors: See details
Setters: An update `LongTableDataMapper` object, returned invisibly.
See Also

Other DataMapper-accessors: DataMapper-accessors, TREDataMapper-accessors

Examples

```r
rowDataMap(exampleDataMapper)
rowDataMap(exampleDataMapper) <- list(c('treatmentid'), c())
colDataMap(exampleDataMapper)
colDataMap(exampleDataMapper) <- list(c('sampleid'), c())
assayMap(exampleDataMapper)
assayMap(exampleDataMapper) <- list(sensitivity=c(viability1='viability'))
metadataMap(exampleDataMapper)
metadataMap(exampleDataMapper) <- list(object_metadata=c('metadata'))
```

LongTableDataMapper-class

A Class for Mapping Between Raw Data and an LongTable Object

Description

A Class for Mapping Between Raw Data and an LongTable Object

Usage

```r
## S4 method for signature 'LongTableDataMapper'
show(object)
```

Arguments

- `object`: A LongTableDataMapper to display in the console.

Value

- `invisible`: Prints to console.

Functions

- `show(LongTableDataMapper)`: Show method for LongTableDataMapper. Determines how the object is displayed in the console.
make_optim_function

Slots
rawdata  See Slots section.
rowDataMap  See Slots section.
colDataMap  See Slots section.
assayMap  See Slots section.
metadataMap  See Slots section.

Slots
- rowDataMap: A list-like object containing two character vectors. The first is column names in rawdata needed to uniquely identify each row, the second is additional columns which map to rows, but are not required to uniquely identify them. Rows should be drugs.
- colDataMap: A list-like object containing two character vectors. The first is column names in rawdata needed to uniquely identify each column, the second is additional columns which map to rows, but are not required to uniquely identify them. Columns should be samples.
- assayMap: A list-like where each item is a list with two elements specifying an assay, the first being the identifier columns in rawdata needed to uniquely identify each row an assay, and the second a list of rawdata columns to be mapped to that assay. The names of assayMap will be the names of the assays in the LongTable that is created when calling metaConstruct on this DataMapper object.
- metadataMap: A list-like where each item is a character vector of rawdata column names to assign to the @metadata of the LongTable, where the name of that assay is the name of the list item. If names are omitted, assays will be numbered by their index in the list.
- rawdata: A list-like object containing one or more pieces of raw data that will be processed and mapped to the slots of an S4 object.
- metadata: A List of object level metadata.

Examples
show(exampleDataMapper)

make_optim_function  Takes a non-primitive R function and refactors it to be compatible with optimization via stats::optim.

Description
Takes a non-primitive R function and refactors it to be compatible with optimization via stats::optim.

Usage
make_optim_function(fn, ...)
**mcc**

Compute a Mathews Correlation Coefficient

### Arguments

- **fn**
  - function A non-primitive function
- ... Arguments to fn to fix for before building the function to be optimized. Useful for reducing the number of free parameters in an optimization if there are insufficient degrees of freedom.

### See Also

- drop_fn_params, collect_fn_params

### Description

The function computes a Matthews correlation coefficient for two factors provided to the function. It assumes each factor is a factor of class labels, and the entries are paired in order of the vectors.

### Usage

```r
mcc(
  x,
  y,
  nperm = 1000,
  nthread = 1,
  alternative = c("two.sided", "less", "greater"),
  ...
)
```

### Arguments

- **x, y**
  - factor of the same length with the same number of levels
- **nperm**
  - numeric number of permutations for significance estimation. If 0, no permutation testing is done
- **nthread**
  - numeric can parallelize permutation texting using BiocParallels bplapply
- **alternative**
  - indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association.
- ... list Additional arguments

### Details

Please note: we recommend you call set.seed() before using this function to ensure the reproducibility of your results. Write down the seed number or save it in a script if you intend to use the results in a publication.
Value

A list with the MCC as the $estimate, and p value as $p.value

Examples

```r
x <- factor(c(1,2,1,2,3,1))
y <- factor(c(2,1,1,1,2,2))
mcc(x,y)
```

mergeAssays

Merge assays with an S4 object.

Description

Merge assays with an S4 object.

Usage

```r
mergeAssays(object, ...)
```

Arguments

- `object` S4 An S4 object a list-like slot containing assays for the object.
- `...` Allow new arguments to be defined for this generic.
mergeAssays, LongTable-method

Value
A modified version of object.

Examples
"This is a generic method!"

mergeAssays, LongTable-method

Endomorphically merge assays within a LongTable or inheriting class

Description
Endomorphically merge assays within a LongTable or inheriting class

Usage
## S4 method for signature 'LongTable'
mergeAssays(object, x, y, target = x, ..., metadata = FALSE)

Arguments
object A LongTable or inheriting class.
x character(1) A valid assay name in object.
y character(1) A valid assay name in object.
target character(1) Name of the assay to assign the result to. Can be a new or existing assay. Defaults to x.
... Fallthrough arguments to merge.data.table to specify the join type. Use this to specify which columns to merge on. If excluded, defaults to by=assayKeys(object, y).
metadata logical A logical vector indicating whether to attach metadata to either assay before the merge occurs. If only one value is passed that value is used for both assays. Defaults to FALSE.

Value
A copy of object with assays x and y merged and assigned to target.

Author(s)
Christopher Eeles

See Also
merge.data.table
**Description**

This method is intended to abstract away complex constructor arguments and data preprocessing steps needed to transform raw data, such as that produced in a treatment-response or next-gen sequencing experiment, and automate building of the appropriate S4 container object. This is intended to allow mapping between different experimental designs, in the form of an S4 configuration object, and various S4 class containers in the Bioconductor community and beyond.

**Usage**

```r
metaConstruct(mapper, ...)  
```

```
## S4 method for signature 'LongTableDataMapper'
metaConstruct(mapper)
```

```
## S4 method for signature 'TREDataMapper'
metaConstruct(mapper)
```

**Arguments**

- `mapper` An `TREDataMapper` object abstracting arguments to an the `TreatmentResponseExperiment` constructor.
- `...` Allow new arguments to be defined for this generic.

**Value**

- An S4 object for which the class corresponds to the type of the build configuration object passed to this method.
- A `LongTable` object, as specified in the mapper.
- A `TreatmentResponseExperiment` object, as specified in the mapper.

**Examples**

```r
data(exampleDataMapper)
rowDataMap(exampleDataMapper) <- list(c('treatmentid'), c())
colDataMap(exampleDataMapper) <- list(c('sampleid'), c())
assayMap(exampleDataMapper) <- list(sensitivity=list(c('treatmentid', "sampleid"), c('viability')))
metadataMap(exampleDataMapper) <- list(experiment_metadata=c('metadata'))
longTable <- metaConstruct(exampleDataMapper)
longTable
```

```r
data(exampleDataMapper)
exampleDataMapper <- as(exampleDataMapper, "TREDataMapper")
```
rowDataMap(exampleDataMapper) <- list(c('treatmentid'), c())
colDataMap(exampleDataMapper) <- list(c('sampleid'), c())
assayMap(exampleDataMapper) <- list(sensitivity=list(c('treatmentid', 'sampleid'), c('viability')))
metadataMap(exampleDataMapper) <- list(experiment_metadata=c('metadata'))
tre <- metaConstruct(exampleDataMapper)
tre

metadata,LongTable-method

*Getter method for the metadata slot of a LongTable object*

**Description**

Getter method for the metadata slot of a LongTable object

**Usage**

```r
## S4 method for signature 'LongTable'
metadata(x)
```

**Arguments**

- `x` The LongTable object from which to retrieve the metadata list.

**Value**

- `list` The contents of the metadata slot of the LongTable object.

metadata<-,LongTable-method

*Setter method for the metadata slot of a LongTable object*

**Description**

Setter method for the metadata slot of a LongTable object

**Usage**

```r
## S4 replacement method for signature 'LongTable'
metadata(x) <- value
```

**Arguments**

- `x` LongTable The LongTable to update
- `value` list A list of new metadata associated with a LongTable object.
Value
LongTable A copy of the LongTable object with the value in the metadata slot.

---

**mutable**
Remove the "immutable" S3-class from an R object, allowing it to be modified normally again.

---

Description
Remove the "immutable" S3-class from an R object, allowing it to be modified normally again.

Usage
```r
mutable(object)
```

Arguments
object An R object inheriting from the "immutable" class.

Value
The object with the "immutable" class stripped from it.

Examples
```r
immut_list <- immutable(list())
mutable(immut_list)
```

---

**nci_TRE_small**
NCI-ALMANAC Drug Combination Data TreatmentResponseExperiment Subset

---

Description
This is a TreatmentResponseExperiment object containing a subset of NCI-ALMANAC drug combination screening data, with 2347 unique treatment combinations on 10 cancer cell lines selected.

Usage
data(nci_TRE_small)

Format
TreatmentResponseExperiment object
References


optimizeCoreGx

A helper method to find the best multithreading configuration for your computer

Description

A helper method to find the best multithreading configuration for your computer

Usage

optimizeCoreGx(sample_data, set = FALSE, report = !set)

Arguments

sample_data  TreatmentResponseExperiment
set  logical(1) Should the function modify your R environment with the predicted optimal settings? This changes the global state of your R session!
report  logical(1) Should a data.frame of results be returned by number of threads and operation be returned? Defaults to !set.

Value

If set=TRUE, modifies data.table threads via setDTthreads(), otherwise displays a message indicating the optimal number of threads. If report=TRUE, also returns a data.frame of the benchmark results.

Examples

data(merckLongTable)
optimizeCoreGx(merckLongTable)
printSlot

Helper function to print slot information

Description

Helper function to print slot information

Usage

printSlot(slotName, slotData)

Arguments

slotName character The name of the slot to print.
slotData data.table The data to print.

reindex

Generic method for resetting indexing in an S4 object

Description

This method allows integer indexes used to maintain referential integrity internal to an S4 object to be reset. This is useful particularly after subsetting an object, as certain indexes may no longer be present in the object data. Reindexing removes gaps integer indexes and ensures that the smallest contiguous integer values are used in an objects indexes.

Usage

reindex(object, ...)

Arguments

object S4 An object to redo indexing for
... pairlist Allow definition of new parameters to this generic.

Value

Depends on the implemented method

Examples

print("Generics shouldn't need examples?")
**reindex, LongTable-method**

Redo indexing for a LongTable object to remove any gaps in integer indexes

---

**Description**

After subsetting a LongTable, it is possible that values of rowKey or colKey could no longer be present in the object. As a result, the indexes will no longer be contiguous integers. This method will calculate a new set of rowKey and colKey values such that integer indexes are the smallest set of contiguous integers possible for the data.

**Usage**

```r
## S4 method for signature 'LongTable'
reindex(object)
```

**Arguments**

- `object` The LongTable object to recalculate indexes (rowKey and colKey values) for.

**Value**

A copy of the LongTable with all keys as the smallest set of contiguous integers possible given the current data.

---

**rowData, LongTableDataMapper-method**

Convenience method to subset the rowData out of the rawdata slot using the assigned rowDataMap metadata.

---

**Description**

Convenience method to subset the rowData out of the rawdata slot using the assigned rowDataMap metadata.

**Usage**

```r
## S4 method for signature 'LongTableDataMapper'
rowData(x, key = TRUE)
```

**Arguments**

- `x` LongTableDataMapper object with valid data in the rawdata and colDataMap slots.
- `key` logical(1) Should the table be keyed according to the id_columns of the rowDataMap slot? This will sort the table in memory. Default is TRUE.
rowData,TREDataMapper-method

Convenience method to subset the rowData out of the rawdata slot using the assigned rowDataMap metadata.

Description
Convenience method to subset the rowData out of the rawdata slot using the assigned rowDataMap metadata.

Usage
## S4 method for signature 'TREDataMapper'
rowData(x, key = TRUE)

Arguments
x  TREDaMapper object with valid data in the rawdata and colDataMap slots.
key  logical(1) Should the table be keyed according to the id_columns of the rowDataMap slot? This will sort the table in memory. Default is TRUE.

Value
data.table The rowData as specified in the rowDataMap slot.

rowIDs

Generic to access the row identifiers from

Description
Generic to access the row identifiers from

Usage
rowIDs(object, ...)

Arguments
object  S4 An object to get row id columns from.
...  Allow new arguments to this generic.
rowMeta

Value

Depends on the implemented method.

Examples

print("Generics shouldn't need examples?")

sensitivityInfo

Generic function to get the annotations for a treatment response experiment from an S4 class

Description

Generic function to get the annotations for a treatment response experiment from an S4 class

Usage

sensitivityInfo(object, ...)

Arguments

object S4 An object to get row metadata columns from.
... Allow new arguments to this generic.

Value

Depends on the implemented method.

Examples

print("Generics shouldn't need examples?")
Arguments

object

An S4 object to get treatment response experiment annotations from.

...

Allow new arguments to be defined for this generic.

Value

Depends on the implemented method

Examples

print("Generics shouldn't need examples?")
Description
Get the names of the sensitivity summary metrics available in an S4 object.

Usage
sensitivityMeasures(object, ...)

Arguments
object An S4 object to retrieve the names of sensitivity summary measurements for.
... Fallthrough arguments for defining new methods

Value
Depends on the implemented method

Examples
sensitivityMeasures(clevelandSmall_cSet)

Description
Set the names of the sensitivity summary metrics available in an S4 object.

Usage
sensitivityMeasures(object, ...) <- value

Arguments
object An S4 object to update.
... Allow new methods to be defined for this generic.
value A set of names for sensitivity measures to use to update the object with.

Value
Depends on the implemented method
## sensitivityProfiles<-  
**sensitivityProfiles Generic**

### Description
A generic for the sensitivityProfiles replacement method

### Usage
```r
sensitivityProfiles(object, ...) <- value
```

### Arguments
- **object**: An S4 object to update the sensitivity profile summaries for.
- **...**: Fallthrough arguments for defining new methods
- **value**: An object with the new sensitivity profiles. If a matrix object is passed in, converted to data.frame before assignment

### Examples
```r
print("Generics shouldn't need examples?")
```
**Description**

Generic function to get the raw data array for a treatment response experiment from an S4 class.

**Usage**

```r
sensitivityRaw(object, ...)```

**Arguments**

- `object` An S4 object to extract the raw sensitivity experiment data from.
- `...` `pairlist` Allow new parameters to be defined for this generic.

**Value**

Depends on the implemented method

**Examples**

```r
print("Generics shouldn't need examples")
```

---

**Description**

Generic function to set the raw data array for a treatment response experiment in an S4 class.

**Usage**

```r
sensitivityRaw(object, ...) <- value```

**Arguments**

- `object` An S4 object to extract the raw sensitivity data from.
- `...` `pairlist` Allow new parameters to be defined for this generic.
- `value` An object containing dose and viability metrics to update the object with.

**Value**

Depends on the implemented method
sensitivitySlotToLongTable

sensitivitySlotToLongTable Generic

Description

Convert the sensitivity slot in an object inheriting from a CoreSet from a list to a LongTable.

Usage

sensitivitySlotToLongTable(object, ...)

Arguments

object CoreSet Object inheriting from CoreSet.
...
Allow new arguments to be defined on this generic.

Value

A LongTable object containing the data in the sensitivity slot.

Examples

print("Generics shouldn't need examples?")

setOps-immutable

Subset an immutable object, returning another immutable object.

Description

Subset an immutable object, returning another immutable object.

Usage

subset.immutable(x, ...)

## S3 method for class 'immutable'
x[...]

## S3 method for class 'immutable'
x[[...]]

## S3 method for class 'immutable'
x$...
**Arguments**

- **x**
  An R object inheriting from the "immutable" S3-class.

- **...**
  Catch any additional parameters. Lets objects with arbitrary dimensions be made immutable.

**Value**

An immutable subset of x.

**Examples**

```r
immut_mat <- immutable(matrix(1:100, 10, 10))
immut_mat[1:5, 1:5]
```

---

**Description**

Show a CoreSet

**Usage**

```r
## S4 method for signature 'CoreSet'
show(object)
```

**Arguments**

- **object**
  CoreSet object to show via `cat`.

**Value**

Prints the CoreSet object to the output stream, and returns invisible NULL.

**See Also**

- `cat`

**Examples**

```r
show(clevelandSmall_cSet)
```
**Description**

Show method for the LongTable class

**Usage**

```r
## S4 method for signature 'LongTable'
show(object)
```

**Arguments**

- `object` A LongTable object to print the results for.

**Value**

`invisible` Prints to console.

**Examples**

```r
show(merckLongTable)
```

---

**showSigAnnot**

*Get the annotations for a Signature class object, as returned by drugSensitivitySig or radSensitivitySig functions available in PharmacoGx and RadioGx, respectively.*

**Description**

Get the annotations for a Signature class object, as returned by drugSensitivitySig or radSensitivitySig functions available in PharmacoGx and RadioGx, respectively.

**Usage**

```r
showSigAnnot(object, ...)
```

**Arguments**

- `object` A Signature class object
- `...` Allow definition of new arguments to this generic

**Value**

`NULL` Prints the signature annotations to console
Examples

print("Generics shouldn't need examples?")

Description

Allows use of the colData and rowData data.table objects to query based on rowID and colID, which is then used to subset all assay data.tables stored in the assays slot. This function is endomorphic, it always returns a LongTable object.

Usage

## S4 method for signature 'LongTable'
subset(x, i, j, assays = assayNames(x), reindex = TRUE)

Arguments

x LongTable The object to subset.

i character, numeric, logical or call Character: pass in a character vector of rownames for the LongTable object or a valid regex query which will be evaluated against the rownames. Numeric or Logical: vector of indices or a logical vector to subset the rows of a LongTable. Call: Accepts valid query statements to the data.table i parameter, this can be used to make complex queries using the data.table API for the rowData data.table.

j character, numeric, logical or call Character: pass in a character vector of colnames for the LongTable object or a valid regex query which will be evaluated against the colnames. Numeric or Logical: vector of indices or a logical vector to subset the columns of a LongTable. Call: Accepts valid query statements to the data.table j parameter, this can be used to make complex queries using the data.table API for the colData data.table.

assays character, numeric or logical Optional list of assay names to subset. Can be used to subset the assays list further, returning only the selected items in the new LongTable.

reindex logical(1) Should index values be reset such that they are the smallest possible set of consecutive integers. Modifies the "rowKey", "colKey", and all assayKey columns. Initial benchmarks indicate reindex=FALSE saves ~20% of both execution time and memory allocation. The cost of reindexing decreases the smaller your subset gets.

Value

LongTable A new LongTable object subset based on the specified parameters.


**Examples**

```r
# Character
subset(merckLongTable, 'ABT-888', 'CAOV3')
# Numeric
subset(merckLongTable, 1, c(1, 2))
# Logical
subset(merckLongTable, colData(merckLongTable)$sampleid == 'A2058')
# Call
subset(merckLongTable, drug1id == 'Dasatinib' & drug2id != '5-FU',
      sampleid == 'A2058')
```

---

**subsetTo**

*Subset a CoreSet object based on various parameters, such as cell lines, molecular features*

---

**Description**

Subset a CoreSet object based on various parameters, such as cell lines, molecular features

**Usage**

```r
subsetTo(object, ...)
```

**Arguments**

- `object` An object inheriting from the CoreGx::CoreSet class
- `...` Allow definition of new arguments to this generic

**Value**

A subsetted version of the original object

**Examples**

"Generics shouldn't need examples!"
**summarizeMolecularProfiles**

*Summarize molecular profile data such that there is a single entry for each sample line/treatment combination*

**Description**

Summarize molecular profile data such that there is a single entry for each sample line/treatment combination

**Usage**

`summarizeMolecularProfiles(object, ...)`

**Arguments**

- `object`: An S4 object to summarize the molecular profiles for.
- `...`: Allow definition of new arguments to this generic

**Value**

Depends on the implemented method

**Examples**

```r
print("Generics shouldn't need examples?")
```

---

**summarizeSensitivityProfiles**

*Summarize across replicates for a sensitivity dose-response experiment*

**Description**

Summarize across replicates for a sensitivity dose-response experiment

**Usage**

`summarizeSensitivityProfiles(object, ...)`

**Arguments**

- `object`: An S4 object to summarize sensitivity profiles for.
- `...`: Allow definition of new arguments to this generic
Value

Depends on the implemented method

Examples

print("Generics shouldn't need examples?")

--------

TreatmentResponseExperiment

_TreatmentResponseExperiment constructor method_

--------

Description

Builds a TreatmentResponseExperiment object from rectangular objects. The rowData argument should contain row level metadata, while the colData argument should contain column level metadata, for the experimental assays in the assays list. The rowIDs and colIDs lists are used to configure the internal keys mapping rows or columns to rows in the assays. Each list should contain at minimum one character vector, specifying which columns in rowData or colData are required to uniquely identify each row. An optional second character vector can be included, specifying any metadata columns for either dimension. These should contain information about each row but NOT be required to uniquely identify a row in the colData or rowData objects. Additional metadata can be attached to a TreatmentResponseExperiment by passing a list to the metadata argument.

Usage

TreatmentResponseExperiment(
  rowData,
  rowIDs,
  colData,
  colIDs,
  assays,
  assayIDs,
  metadata = list(),
  keep.rownames = FALSE
)

Arguments

rowData data.table, data.frame, matrix A table like object coercible to a data.table containing the a unique rowID column which is used to key assays, as well as additional row metadata to subset on.

rowIDs character, integer A vector specifying the names or integer indexes of the row data identifier columns. These columns will be pasted together to make up the rownames of the TreatmentResponseExperiment object.
colData | data.table, data.frame, matrix A table like object coercible to a data.table containing the a unique colID column which is used to key assays, as well as additional column metadata to subset on.

colIDs | character, integer A vector specifying the names or integer indexes of the column data identifier columns. These columns will be pasted together to make up the colnames of the TreatmentResponseExperiment object.

assays | A list containing one or more objects coercible to a data.table, and keyed by rowIDs and colIDs corresponding to the rowID and colID columns in colData and rowData.

assayIDs | list A list of character vectors specifying the columns needed to uniquely identify each row in an assay. Names must match the assays list.

metadata | A list of metadata associated with the TreatmentResponseExperiment object being constructed

keep.rownames | logical, character Logical: whether rownames should be added as a column if coercing to a data.table, default is FALSE. If TRUE, rownames are added to the column 'rn'. Character: specify a custom column name to store the rownames in.

Details

For now this class is simply a wrapper around a LongTable class. In the future we plan to refactor CoreGx such that the LongTable class is in a separate package. We can then specialize the implementation of TreatmentResponseExperiment to better capture the biomedical nature of this object.

Value

A TreatmentResponseExperiment object containing the data for a treatment response experiment configured according to the rowIDs and colIDs arguments.
TREDataMapper

Slots

  rowData  See Slots section.
  colData  See Slots section.
  assays   See Slots section.
  metadata See Slots section.
  .intern  See Slots section.

Slots

  • rowData: A data.table containing the metadata associated with the row dimension of a TreatmentResponseExperiment.
  • colData: A data.table containing the metadata associated with the column dimension of a TreatmentResponseExperiment.
  • assays: A list of data.tables, one for each assay in a TreatmentResponseExperiment.
  • metadata: An optional list of additional metadata for a TreatmentResponseExperiment which doesn’t map to one of the dimensions.
  • .intern: An environment that holds internal structural metadata about a TreatmentResponseExperiment object, such as which columns are required to key the object. An environment has been used to allow locking items, which can prevent accidental modification of a property required for the class to work.

TREDataMapper  Constructor for the TREDataMapper class, which maps from one or more raw experimental data files to the slots of a LongTable object.

Description

Constructor for the TREDataMapper class, which maps from one or more raw experimental data files to the slots of a LongTable object.

Usage

TREDataMapper(
  rawdata = data.frame(),
  rowDataMap = list(character(), character()),
  colDataMap = list(character(), character()),
  assayMap = list(list(character(), character())),
  metadataMap = list(character())
)
Arguments

rawdata  
A data.frame of raw data from a treatment response experiment. This will be coerced to a data.table internally. We recommend using joins to aggregate your raw data if it is not present in a single file.

rowDataMap  
A list-like object containing two character vectors. The first is column names in rawdata needed to uniquely identify each row, the second is additional columns which map to rows, but are not required to uniquely identify them. Rows should be treatments.

colDataMap  
A list-like object containing two character vectors. The first is column names in rawdata needed to uniquely identify each column, the second is additional columns which map to rows, but are not required to uniquely identify them. Columns should be samples.

assayMap  
A list-like where each item is a list with two character vectors defining an assay, the first containing the identifier columns in rawdata needed to uniquely identify each row an assay, and the second the rawdata columns to be mapped to that assay. The names of assayMap will be the names of the assays in the TreatmentResponseExperiment that is created when calling metaConstruct on this DataMapper object. If the character vectors have names, the value columns will be renamed accordingly.

metadataMap  
A list-like where each item is a character vector of rawdata column names to assign to the @metadata of the LongTable, where the name of that assay is the name of the list item. If names are omitted, assays will be numbered by their index in the list.

Details

The guessMapping method can be used to test hypotheses about the cardinality of one or more sets of identifier columns. This is helpful to determine the id columns for rowDataMap and colDataMap, as well as identify columns mapping to assays or metadata.

To attach metadata not associated with rawdata, please use the metadata assignment method on your TREDataMapper. This metadata will be merge with any metadata from metadataMap and added to the LongTable which this object ultimately constructs.

Value

A TREDataMapper object, with columns mapped to it’s slots according to the various maps in the LongTableDataMapper object.

See Also

guessMapping
TREDataMapper-accessors

Accessing and modifying data in a TREDataMapper object.

Description

Documentation for the various setters and getters which allow manipulation of data in the slots of a TREDataMapper object.

Usage

```r
## S4 replacement method for signature 'TREDataMapper,list'
rawdata(object) <- value

## S4 method for signature 'TREDataMapper'
rowDataMap(object)

## S4 replacement method for signature 'TREDataMapper,list_OR_List'
rowDataMap(object) <- value

## S4 method for signature 'TREDataMapper'
colDataMap(object)

## S4 replacement method for signature 'TREDataMapper,list_OR_List'
colDataMap(object) <- value

## S4 method for signature 'TREDataMapper'
assayMap(object)

## S4 replacement method for signature 'TREDataMapper,list_OR_List'
assayMap(object) <- value

## S4 method for signature 'TREDataMapper'
metadataMap(object)

## S4 replacement method for signature 'TREDataMapper,list_OR_List'
metadataMap(object) <- value
```

Arguments

- **object**: A TREDataMapper object to get or set data from.
- **value**: See details.

Details

- **rawdata**: Get the raw data slot from a TREDataMapper object. Returns a list-like containing one or more raw data inputs to the TREDataMapper object.
rawdata: Set the raw data slot from a TREDataMapper object. value: The list-like object to set for the rawdata slot. Note: this currently only supports data.frame or data.table objects.

rowDataMap: list of two character vectors, the first are the columns required to uniquely identify each row of a TREDataMapper and the second any additional row-level metadata. If the character vectors have names, the resulting columns are automatically renamed to the item name of the specified column.

rowDataMap<-: Update the @rowDataMap slot of a TREDataMapper object, returning an invisible NULL. Arguments:

• value: A list or List where the first item is the names of the identifier columns – columns needed to uniquely identify each row in rowData – and the second item is the metadata associated with those the identifier columns, but not required to uniquely identify rows in the object rowData.

colDataMap: list of two character vectors, the first are the columns required to uniquely identify each row of a TREDataMapper and the second any additional col-level metadata. If the character vectors have names, the resulting columns are automatically renamed to the item name of the specified column.

colDataMap<-: Update the @colDataMap slot of a TREDataMapper object, returning an invisible NULL. Arguments:

• value: A list or List where the first item is the names of the identifier columns – columns needed to uniquely identify each row in colData – and the second item is the metadata associated with those the identifier columns, but not required to uniquely identify rows in the object rowData.

assayMap: A list of character vectors. The name of each list item will be the assay in a LongTableDataMapper object that the columns in the character vector will be assigned to. Column renaming occurs automatically when the character vectors have names (from the value to the name).

assayMap<-: Updates the @assayMap slot of a TREDataMapper object, returning an invisible NULL. Arguments:

• value: A list of character vectors, where the name of each list item is the name of an assay and the values of each character vector specify the columns mapping to the assay in the S4 object the TREDataMapper constructs.

metadataMap: A list of character vectors. Each item is an element of the constructed objects @metadata slot.

metadataMap<-: Updates TREDataMapper object in-place, then returns an invisible(NULL). Arguments:

• value: A list of character vectors. The name of each list item is the name of the item in the @metadata slot of the TREDataMapper object created when metaConstruct is called on the DataMapper, and a character vector specifies the columns of @rawdata to assign to each item.

Value

Accessors: See details
Setters: An update TREDataMapper object, returned invisibly.
TREDataMapper-class

A Class for Mapping Between Raw Data and an TreatmentResponseExperiment Object

Description

A Class for Mapping Between Raw Data and an TreatmentResponseExperiment Object

Slots

- rowData  See Slots section.
- rowDataMap  See Slots section.
- colDataMap  See Slots section.
- assayMap  See Slots section.
- metadataMap  See Slots section.

Slots

- rowDataMap: A list-like object containing two character vectors. The first is column names in rawdata needed to uniquely identify each row, the second is additional columns which map to rows, but are not required to uniquely identify them. Rows should be drugs.
- colDataMap: A list-like object containing two character vectors. The first is column names in rawdata needed to uniquely identify each column, the second is additional columns which map to rows, but are not required to uniquely identify them. Columns should be samples.
• assayMap A list-like where each item is a list with two elements specifying an assay, the first being the identifier columns in rawdata needed to uniquely identify each row an assay, and the second a list of rawdata columns to be mapped to that assay. The names of assayMap will be the names of the assays in the LongTable that is created when calling metaConstruct on this DataMapper object.

• metadataMap: A list-like where each item is a character vector of rawdata column names to assign to the @metadata of the LongTable, where the name of that assay is the name of the list item. If names are omitted, assays will be numbered by their index in the list.

• rawdata: A list-like object containing one or more pieces of raw data that will be processed and mapped to the slots of an S4 object.

• metadata: A List of object level metadata.

---

**updateObject,CoreSet-method**

*Update the CoreSet class after changes in its structure or API*

**Description**

Update the CoreSet class after changes in its structure or API

**Usage**

```r
## S4 method for signature 'CoreSet'
updateObject(object, verify = FALSE, verbose = FALSE)
```

**Arguments**

- **object** A CoreSet object to update the class structure for.
- **verify** A logical(1) indicating is validObject should be called after updating the object. Defaults to TRUE, only set FALSE for debugging.
- **verbose** TRUE or FALSE, indicating whether information about the update should be reported

**Value**

CoreSet with update class structure.
**updateObject, LongTable-method**

*Update the LongTable class after changes in its structure or API*

**Description**

Update the LongTable class after changes in its structure or API

**Usage**

```r
## S4 method for signature 'LongTable'
updateObject(object, verify = FALSE, verbose = FALSE)
```

**Arguments**

- `object`: A LongTable object to update the class structure for.
- `verify`: A logical(1) indicating if `validObject` should be called after updating the object. Defaults to TRUE, only set FALSE for debugging.
- `verbose`: TRUE or FALSE, indicating whether information about the update should be reported

**Value**

LongTable with updated class structure.

---

**updateSampleId**

*Update the sample ids in a cSet object*

**Description**

Update the sample ids in a cSet object

**Usage**

```r
updateSampleId(object, new.ids = vector("character"))
```

**Arguments**

- `object`: The object for which the sample ids will be updated
- `new.ids`: The new ids to assign to the object

**Value**

CoreSet The modified CoreSet object
Examples

updateSampleId(clevelandSmall_cSet, sampleNames(clevelandSmall_cSet))

updateTreatmentId(clevelandSmall_cSet, treatmentNames(clevelandSmall_cSet))

Description

Update the treatment ids in a cSet object

Usage

updateTreatmentId(object, new.ids = vector("character"))

Arguments

object The object for which the treatment ids will be updated
new.ids The new ids to assign to the object

Value

CoreSet The modified CoreSet object

Examples

updateTreatmentId(clevelandSmall_cSet, treatmentNames(clevelandSmall_cSet))
Arguments

- **x**
  - LongTable The object to subset.

- **i**
  - character, numeric, logical or call Character: pass in a character vector of drug names, which will subset the object on all row id columns matching the vector. This parameter also supports valid R regex query strings which will match on the colnames of x. For convenience, * is converted to .* automatically. Colon can be to denote a specific part of the colnames string to query. Numeric or Logical: these select based on the rowKey from the rowData method for the LongTable. Call: Accepts valid query statements to the data.table i parameter as a call object. We have provided the function .() to conveniently convert raw R statements into a call for use in this function.

- **j**
  - character, numeric, logical or call Character: pass in a character vector of drug names, which will subset the object on all drug id columns matching the vector. This parameter also supports regex queries. Colon can be to denote a specific part of the colnames string to query. Numeric or Logical: these select based on the rowID from the rowData method for the LongTable. Call: Accepts valid query statements to the data.table i parameter as a call object. We have provided the function .() to conveniently convert raw R statements into a call for use in this function.

- **assays**
  - character Names of assays which should be kept in the LongTable after subsetting.

- **drop**
  - logical Included for compatibility with the ’[’ primitive, it defaults to FALSE and changing it does nothing.

Details

This function is endomorphic, it always returns a LongTable object.

Value

A LongTable containing only the data specified in the function parameters.

Examples

```r
# Character
merckLongTable["ABT-888", "CAOV3"]
# Numeric
merckLongTable[1, c(1, 2)]
# Logical
merckLongTable[, colData(merckLongTable)$sampleid == 'A2058']
# Call
merckLongTable[
  .(drug1id == 'Dasatinib' & drug2id != '5-FU'),
  .(sampleid == 'A2058'),
]
```
Method for LongTable Class

Description

Just a wrapper around assay<- for convenience. See '?assay<-,LongTable,character-method'.

Usage

```r
## S4 replacement method for signature 'LongTable,ANY,ANY'
x[[i]] <- value
```

Arguments

- **x**: A LongTable to update.
- **i**: The name of the assay to update, must be in assayNames(object).
- **value**: A data.frame

Value

A LongTable object with the assay i updated using value.

Examples

```r
merckLongTable[["sensitivity"]]<- merckLongTable[["sensitivity"]]
```

Select an assay from a LongTable object

Description

Select an assay from a LongTable object

Usage

```r
## S4 method for signature 'LongTable'
x$name
```

Arguments

- **x**: A LongTable object to retrieve an assay from
- **name**: character The name of the assay to get.
Value

data.frame The assay object.

Examples

merckLongTable$sensitivity

$<-,LongTable-method

Update an assay from a LongTable object

Description

Update an assay from a LongTable object

Usage

## S4 replacement method for signature 'LongTable'
x$name <- value

Arguments

x A LongTable to update an assay for.
name character(1) The name of the assay to update
value A data.frame or data.table to update the assay with.

Value

Updates the assay name in x with value, returning an invisible NULL.

Examples

merckLongTable$sensitivity <- merckLongTable$sensitivity
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